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Fri Mar
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

US-09-236-995D-3

1 aacaagatgctattatggca......gtttccatcacaagaggtag 474 Perfect score: Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

2944280 1472140 seqs, 8248589755 residues Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmb1:* Database :

gb_ow:*
gb_pat:*
gb_ph:*
gb_p1:*
gb_p1:*
gb_p7:* gb_vi:* em_ba:* em_fun:* gb_ba:* gb_htg:* gb_in:* gb_sy:*

em_pat:* em_hum:* em_sts:* em_om:* em_or:* em_in:* em_ro:* em_un:* em_p1:* em_sy:* em_ov:* 14: 115: 116: 117: 119: 220: 221: 224: 224: 30:

em_htgo_num: em_htgo_rod: em_htg_hum: em_htg_inv: em_htg_inv: em_vi:* em_htgo_hum:*

em_htg_other:*

Description	589 Zea	_	AJ131705 Arabidops	1040	DI466/ Frog mknA r	rattus	Z12139 X. Laevis PA	A.thaile	Chicker	J Mu	AJ222588 Zea mays	X14206 Mouse mRNA			781 Cri	Human		U	Human p	ဗ	O Seque	AX062277 Sequence	M32721 Human poly(I14359 Sequence 5	AF051548 Drosophil		Fruit fly		O	AC014613 Drosophil		^	7	Se	ď	80	Sedne	12	9283	317	3892	5837	583	AF085734 Homo sapi	AX058338 Sequence
ID	ZMPARP2	AF093627	ATH131705	KNPAKPZ	≃ ⋅	KNU94340	XLPARPG	ATPARP	GGPADPRP	BC012041	ZMPARP1	MMADPRP	BOVPAS	AF126717	AF168781	HUMADPPO	HUMPOLP	A52134	HUMRISDAD	GORADPRB	AX058340	AX062277	HUMPPOL	114359	DMPARP5	S54638	DROADPRPA	114360	HUMPADPRPZ	AC014613	AE002892	AL442128	SPEPADPRP	114357	38	3	3	9	HSA236876	AX058317	389	7	AX058362	AF085734	05
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Result No.	-	2	e -	4	S.	9	7	80	δ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	c 30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. ZMPARP2 3211 bp mRNA PLN 19-NOV-1997 Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp). AJ222589 1 (bases 1 to 3211)
Bablychuk,E., Cottrill,D., Storozhenko,S., Fuangthong,M., O'Farrell,M., Van Montagu,M., Inze,D. and Rushnir,S. Higher plants possess two poly(ADP-ribose) polymerases unpublished AJ222589.1 GI:2632128 PARP gene; poly(ADP-ribose) polymerase: Zea mays. Zea mays DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS RESULT ZMPARP2

Z (bases 1 to 3211) Kushnir, S. Direct Submission JOURNAL REFERENCE AUTHORS TITLE TITLE

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Fri

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GEMPMANHASVDDVEGIDALRWDDGEGIRNYGSASAGATSTRAPPERCTIELAPSAR
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KNDYLMKWFKSQKVKKPERVLPPMSPEKSGSKATQRTSLLSSKGLDKLRFSYVGGSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                              AANEWIEKLKLAGANFYARVVKDIDCLIACGELDNENAEVRKARRLKIPIVREGYIGE
CVKKNKMLPFDLYKLENALESSKGSTVTVKVKGRSAVHESSGLQDTAHILEDGKSIYN
ATLNMSDLALGVNSYYVLQIIEQDDGSECYVFRKWGRVGSEKIGGGKLEEMSKTEAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFKRLFLEKTGNSWEAWEČKTNFRKOPGRFYPLDVDYGVKKAPKRĎISEMKSSLAPO
LLELMKMLFNVETYRAAMMEPEINMSEMPLGKLSKENIEKGFEALTEIONLLKDTADO
ALAVRESLIVAASNRFFTLIPSIHPHIIRDEDDLMIKAKMLEALQDIEIASKIVGFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GELNKYSRYKNNLHNKMLLMHGSRLTNFVGILSQGLRIAPPEAPVTGYMFGKGLYFAD
LVSKSAQYCYVDRNNPVGLMLLSEVALGDMYELKKATSMDKPPRGKHSTKGLGKTVPL
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     Dep. Genetics
                                                                                                                                                                                               /function="secondary protein modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                     /product="poly(ADP-ribose) polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 474; DB 8; I
llarity 100.0%; Pred. No. 9.2e-139;
Conservative 0; Mismatches 0;
 S., VIB,
Belgium
                                                                                                                                                                                                                                                     /protein_id="CAA10889.1"
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/db_xref="SPTREMBL:024570"
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                   Ledeganckstraat 35, Gent, B9000,
Location/Qualifiers
Submitted (14-NOV-1997) Kushnir
                                                                                             /db_xref-"taxon:4577"
                                                                             /organism="Zea mays"
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                                                                                                                 113. .3022
/gene="PARP"
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/gene="PARP"
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Matches 474;
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/translation="MAAPPKAWKAFYAKSGRASCKSCRSPIAKDQLRLGKMVQASQFD
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KCTIEIAPSARTSCRRCSEKITKGSVRLSAKLESEGPKGIPWYHANCFFEVSPSATVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRESVVGOSKEAANEWIEKLKLÄGANFYARVVKDIDCLIACGELDNENAEVRKARRLK
IPIVREGYIGECVKKNKMLPFDLYKLENALESSKGSTVTVKVKCRSAVHESSGLODTA
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TASKIVGRDSBOBSILDKYMKLHCDITPLAHDSEDYKLIEQYLLNTHAPTHKDWSL
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YMFGKGLYFADLVSKSAQYCYVDRNNPYGLMLLSEVALGDMYELKKATSHDK PPRGKH
                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.

1 (bases 1 to 3285)
Mahajan, P. B. and Zuo, Z.
Purification and cDNA cloning of maize Poly(ADP)-ribose polymerase Plant Physiol. 118 (3), 895-905 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFSGWDTLSDEDKRTMLDLVKKDVGNNEQNKGSKRKKSENDIDSYKSARLDESTSEGT
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VKKKWQ1PHGTKNDYLMKWFKSQKVKKPERVLPPMSPEKSGSKATQRTSLLSSKGLDK
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                                                                                                                                                                                                                Embryophyta; Tracheophyta;
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Submitted (22-SEP-1998) Crop Protection, Pioneer Hibred
International, Inc., 7300 NW 62nd Avenue, Johnston, IA 50131-1004,
USA
                          AF093627 3285 bp mRNA PLN 29-NOV-1998.
Zea mays poly(ADP)-ribose polymerase (PARP1) mRNA, complete cds.
AF093627
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100.0%; Pred. No. 9.3e-139;
tive 0; Mismatches 0;
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/organism="Zea
                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 3285)
Mahajan, P.B. and Zuo, Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="PARP1"
100. .3042
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Best Local S
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                                                                DEFINITION
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AUTHORS
                                                                                             ACCESSION
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                       AF093627
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LEMSSSTELEELSGGRESI PDSDQEALLPLYKKALPAKTETAEAROTNSRAGTKRKND
SVDNEKSKLAKSSFDMSTSGALQPCSKEKENEAQYRELMDLKDDLKKYUTSAELREML
EVNDGSTROSELDLADDKGADOMFGPLALCPUGSGHLSFSGGLYRCHGY I SEWSKCSH
STLDPDRTKCKWI PDETENOPLIKWNKSOKSYKPRILIRPYLSGETSQGGGSKDATD
SSRSERLADLKVSIAGNTKEROPWKKRIEEAGAEFHANVKKGTSCLVVCGLTDIRDAE
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TSSTANNAKLEYGIEVSQTSRAGCRKCSEKILKGEVRIFSKPEGPGNKGLMWHHAKCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 3187)
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Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie
Vegetale Et De Microbiologie, Commissariat A L'energie Atomique,
CEA Cadarache, Lab. De Radiobiol. Vegetale, Bat. 185, 13108 St.
Paul.les-Durance, FRANCE
2 (bases 1 to 3187)
2689 TACTTTGCAGATCTAGTAAGCAAGCGCACAATACTGTTATGTGGATAGGAATAATCCT 2748
                                                                                                360
                                                                                                                                                                                                                                                                                                                                                420
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                                                                                                                                                            241 acgtccatggacaaacctccaagagggaagcattcgaccaagggattaggcaaaaccgtg 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAD(+) ADP-ribosyltransferase; parp-1 gene; poly(ADP-ribose)
                                                                     2929 GTGCCATCAATTAGGAGCTCTGAACTCATGTACAATGAGTACATCGTCTACAACACA
                                                                                                                                                                                                                                                         301 ccactggagtcagagtttgtgaagtggaagggatgatgtcgtagttccctgcggcaagccg
                                                                                                                                                                                                                                                                                                                                                361 gtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name="NAD(+) ADP-ribosyltransferase"
/BC_number="2,42.30"
/Inction="ADD-Ribose polymer synthesis"
/note="mol. weight: 111 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="poly(ADP-ribose) polymerase"
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/db_xref="G1:4038491"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
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/gene="par
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Thibodeau, J., Gradwohl, G., Dumas, C., Clairoux-Moreau, S., Brunet, G., Penning, C., Poirier, G.G. and Moreau, P. Cloning of rodent cDNA coding the poly(ADP-ribose) polymerase catalytic domain and analysis of mRNA levels during the cell cycle Biochem. Cell Biol. 67 (9), 653-660 (1989)
                                                                                                                                  WSLELEEVFALEREGEFDKYAPHREKLGNKMLLWHGSELTNFYGILNOGLRIAPPEAP
ATGYMFGKGIYFADLNSKSAQYCYTCKKNPYGLMLLSEVALGEIHELTKAKYMDKPPR
GKHSTKGLGKKVPQDSEFAKWRGDVTVPCGKPVSSKVKASELMYNEYIVYDTAQVKLO
                                                                                                ALTEIQRLLTESDPQPTMKESLLVDASNRFFTMIPSIHPHIIRDEDDFKSKVKMLEAL
                                                                                                                   QDIEIASRIVGFDVDSTESLDDKYKKLHCDISPLPHDSEDYRLIEKYLNTHAPTHTE
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                                                                       AKKEPFQTSSNLAPSLIELMKMLFDVETYRSAMMEFEINMSEMPLGKLSKHNIQKGFE
MRKARRMKVAIVKEDYLVDCFKKQRKLPFDKYKIEDTSESLVTVKVKGRSAVHEASGL
QEHCHILEDGNSIYNTTLSMSDLSTGINSYYILQIJQEDKGSDCYVFRKWGRVGNEKI
                                                 GGNKVEEMSKSDAVHEFKRLFLEKTGNTWESWEQKTNFQKQPGKFLPLDIDYGVNKQV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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R.norvegicus mRNA for poly(ADP-ribose) polymerase (clone pRATC).
X65497
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                                                                                                                                                                                                                                                                                                               /product="poly(ADP-ribose) polymerase"
                                                                                                                                                                                                                                                                /gene="parp-1"
/EC_number="2.4.2.30"
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/product="Poly(ADP-ribose) polymerase"
/protein_id="CA446478.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AWHSKNFTKYPKFHPLAIDYGQDEEAVKKLAVKPGTKSKLPKPVQELVGMIFDVESM
KRALVEVEIDLOKMPLGKLSRRQIQAAYSILESGVQAVSQSSSESQLIDLSNRFTYLI
PHDFGAWKRPELLDWIDSVQAKVEMLDNLLDIEVAS SLLKGGSDDSSKDPIDVNYEKLK
TÜLKVVDRDSEEBAEVIRKYVKNTHATTHNAYDLEVIDIFKIEREGESQRYKPFROLHN
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PIGLILLGEVALGNMYELKHASHISKLPKGKHSVKGLGKTAPDPSASITLDGVEVPLG
TGIPSGVNDTCLLYNEYIVYDIAQVNLKYLLKIKFNFKTSLW"
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                                                                                                               Submitted (23-MAR-1992) F. Potvin, Molecular Endocrinology, CHUL Research Center, 2705, Boul Laurier, Ste-Foy, Quebec, GIV 4G2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1091 GGTCTGCGGATAGCCCCACCTGAAGCACCTGTGACAGGCTACATGTTTGGGAAAGGAATC 1150
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/clone_lib="lambda EMBL4"
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/db_xref="taxon:10116"
/chromosome="1q41-42"
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32. .1510
                        (bases 1 to 1939)
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Submitted (15-MAR-1993) to the DDBJ/EMBL/GenBank databases.
Kazuhiko Uchida, Institute of Basic Medical Sciences, Department of Basichemistry; Ten-noudai 1-1-1, Tsukuba, Ibaraki 305, Japan (E-mail:Kzuchida@md.tsukuba.ac.jp, Tel:0298-53-3271, Fax:0298-53-3039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolation of the poly(ADP-ribose) polymerase-encoding cDNA from Xenopus laevis: phylogenetic conservation of the functional domains Gene 137 (2), 293-297 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolation of Poly(ADP-ribose) Polymerase cDNAs from Xenopus laevis and Cherry Salmon using heterologous oligonucleotide consensus sequences: gene conservation in amphibia, fish, and insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 3718)
Uchida, K., Uchida, M., Hanai, S., Ishikawa, K., Ozawa, Y., Ueno, N. and
                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 3718) Uchida, M., Hanai, S., Ozawa, Y., Ami, Y., Kushida, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2717 AATTGCTCCGCCAGAAGCTCCTGTTACCGGGTATATGTTTGGCAAAGGTATCTTTGC 2776
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                                         04-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //standard_name="Xenopus poly(ADP-ribose) polymerase"
798 c 954 g 861 t
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poly (ADP-ribose) polymerase.
Xenopus laevis egg, oocytes, germ cell, cDNA to mRNA, clone
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0; Mismatches 179;
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Submitted (15-MAR-1993) to DDBJ by:
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0298-53-3039.
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/cell_type="Germ cell"
/dev_stage="Egg"
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1. .3718
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Institute of Basic Medical
University of Tsukuba
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1 (bases 1 to 3718)
Uchida, K.
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TCFVKNRDELGFRPEYSASOLKGFSLLSAEDKEALKKOLPAVKSEGKRKCDEVDGIDE
VAKKKSKKGKDKESSKLEKALKAQNELVWNIKDELKKACSTNDLKELLIFNQOQVPSG
ESAILDRVADGMAFGALLPCKECSGQLVFKSDAYYCTGDVTAWTKCMVKTQNPSRKEW
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DGKVPHWYHFSCFWKVGHSIRQPDTEVDGFSELRWDDQQKVKKTAEAGGVAGKGQHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beneke, S., Meyer, R. and Burkle, A. Isolation of cDNA encoding full-length rat (Rattus norvegicus) poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNU94340 3128 bp mRNA ROD 19-FEB-1998
Rattus norvegicus poly(ADP-ribose) polymerase mRNA, complete cds.
094340
                                                                                                  2897 TACAAAACTTCCCAAGGGCAAACACAGTGTAAAGGGTTTGGGTAGAACTGCACCAGATCC 2956
                                                                                                                                                                                                                                                                                                            2957 CICAGCIACTGIACA --- GCIGGAIGGAGGAGGIGCAICTICTCGGGAAGGAACTICTGC 3013
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                                                                                                                                                                   249 ggacaaacetecaagagggaagcattegaecaagggattaggeaaaaeegtgeeaetgga 308
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                                                                     189 gatgettettetgaggttgetttaggagacatgtatgaactaaagaaagcaegteeat 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-MAR-1997) Angewandte Tumorvirologie, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 242, Heidelberg
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Sequence update by submitter
On Feb 19, 1998 this sequence version replaced gi:2583143.
Location/Qualifiers
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/protein_id="AAC53544.1"
/db_xref="GI:2896792"
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31. .3075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3074 CAACCTGAAGTACCTGCTGAAGCTCAAGTTCAACTACAAG 3113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    429 gaagatgcagttcttgctgaaggtgcgtttccatcacaag 468
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Direct Submission
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AWHSKNETKY PRKET YPLEID YGGDEBAVKKLAVKPGTKSKLPRPYDEHPWKLYTEERTON
KKALVEFEIDLOKMPLGKLSRRQIOAATSILESPYQASVGSSESQLIDLSNRFYTLI
PHDFGMKRPPLLNNTDSVQAKVFMLDNLLDIEVASTLLKGGSDBSKDPIDVNYEKLK
TDIKVVDRDSEBARVIRKY KKNHHATTHNAYDLEVIDIFKIEREGESORK PFRQLHN
RRLLMHGSTRTRRAGILSQGLRIAPPRAPRYCYGYMFGKGITFADMVSKSANYCHTSQD
PTGLILLGEVALGNMYELKHASHISKLPKGKHSYKGLGKTAPDPSASITLDGVEVPLG
PTGLILLGEVALGNMYELKHASHISKLPKKFRFKTSLW"
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de Rennes I. URA CNRS 256
VTPKEFREISYLKKLKIKKODRLFPPESSAPAPPAPPVSITSAPTAVNSSAPADKPLS
NMKILTLGKLSONKDEAKAMIEKLGGKLIGSANKASLCISTKKEVEKMSKKMEEVKAA
NVRVVCEDFLQDVSASAKSLQELLSAHSLSSMCAEVKVEPGEVVVPKGKSAAPSKKSK
GAVKEGGVNKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKGGKVFSATLGLVDIVKGT
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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59.9%; Pred. No. 1.7e-30;
tive 0; Mismatches 185; Indels
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African clawed frog.
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Direct Submission Submitted (15-MAY-1992) Saulier-le Drean B.M., Lab. de Biol. et

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du Developpement, Universite de Rennes I. URA CNRS 256, de Beaulieu, Av. du Gal LeClerc, Rennes-cedex, FRANCE, 35042
                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="poly ADP-ribosylation, DNA repair"
/note="Protein sequence is in conflict with the conceptual
translation; poly(ADP-ribose) polymerase"
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="AKSGRASCKKCGDNIAKESLGLAIMVOSPMFDGKVPHWHHYSCF
WARAPKLSGODIYGYTELRWEDOEMTKAIETGGAAAGAGGDSKGGKGEMTLNDFAAE
WARAPRASCOINGEOTIEKGOIRISKKSVDVERPPOLGMIDRWHPDCPVSSREEDFLP
SYSASOLKGFTILZABENDSLKKKLPAVKNEGKKADEDYDGHSAATKKKIKKEKEKE
SYSASOLKGFTILZABENDSLKKKLPAVKNEGKKADEDYDGHSAATKKKIKKEKEKE
KLEKLLKEQTELIWHIKDELKKVCSTNDLKELLIANKQQVESGETNIVDRYSDGMAFG
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KFKHHDRAFPPCAAPTPISPPAAPEPKPTVEETFPEGKELTNTKVLLIGKLSKKKKKE
KTLIEGLGGKVAGSAHKANLCISTNKEVKKMSKKMEEVKAANVRVVSDDFLKEVESGK
KYQELLGGGTSSWGREIKQBAVQPTEKQPSSGFVAGKSSGKVKEEKGSNKSEKKKKL
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WVFRSWGRVGTVIGSKKLEEMSSKEDAIEHFLNLYQDKTGNNWHSPNFTKYPKKFYPL
EIDYGQEEDVVKKLSVGAGTKSKLAKPVQELIKLIFDVESMKKAMVEFEIDLQKMPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLSKRQIQSAYSILSQVQQAVSESLSBARLLDLSNQFYTLIPHDFGMKKPPLLNNLEY
IQAKVQMLDNLLDIEVAYSLLRGGADDGEKDPIDVKYEKIKTDIKVVAKDSEESRIIC
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SQCLRIAPPEAFYIGYMEGKGIYFADMYSKSANYCHAMPGSPIGLILLGEVALGNMHE
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                                                                                                                                                                                                                                                 _lib="oligo dr primed lambda gt10 library of D.
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Pred. No. 7.3e-38;
0; Mismatches 180;
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                                                                                          /organism⇒"Xenopus laevis"
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/db_xref="GI:1334661"
                                                                                                                                                                                                                                                                                              /clone="clone parp 923"
                                                                                                                /db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                               /EC_number="2.4.2.30"
                                                                                                                                                                                                           /tissue_type="Ovary"
/cell_type="Oocyte"
                                               Location/Qualifiers
                                                                                                                                                                                       /dev_stage="Adult"
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/translation="MankLkVDELRLKIAERCLSTTGVKAVLVERLEBAIAEDTKKEE
SKSKRKRNSSNDTYESNKLIAIGEFRGMIVKELREBAIKRGLDTTGTKKDLLERLCND
ANNVSNAPVKSSNGTDEAEDDNNGFEEEKKEEKISTATKKGAAVLDQMIPDEIKSQYH
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SSSSEVKPEGSKLDTRVAKFISLICNVSMMAOHMMEIGYNANKLPLGKISKSTISKGY
EVLKRISEVIDRYDRTRLEELSGEFYTVIPHDFGFKKMSQFVIDTPQKLKQKIEMVEA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-FEB-1995) Lepiniec L., University Gent, Laboratorium Genetica, 35 KL Ledeganckstraat, GENT, Belgium, B-9000
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PPGKLSTKGVGKTAPNPSEAQTLEDGVVVPLGKPVERSCSKGMLLYNEYIVYNVEQIK
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SGTTVETAQLFRASRAVEADRFPQFSSSKNRMLLWHGSRLTNWAGILSQGLRIAPPEA
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                                                                                    2763 TACAAAACTICCCAAGGGCAAACACAGTGTAAAGGGTTIGGGTAGAACTGCACAGATCC 2822
                                                                                                                                                                                                                                                              2823 CTCAGCTACTGTACA---GCTGGATGGAGGGATGTTCCTCTCGGGAAAGGAACTTCTGC 2879
                                                                                                                                                                                                                                                                                                                                                                                                            249 ggacaaactccaagagggaagcattcgaccaagggattaggcaaaaccgtgccactgga 308
                                                                                                                                                                         309 gtcagagtttgtgaagtggagggatgatgtgtcgtagttccctgcggcaagccggtgccatc 368
                                                                                                                                                                                                                                                                                                                                                             369 atcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacacatcccaggt 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2940 CAACCTGAAGTACCTGCTGAAGCTCAAGTTCAACTACAA 2978
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A.thaliana PARP mRNA for PARP protein.
248243
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/protein_id="CAA88288.1"
/db_xref="G1:853722"
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PARP gene; PARP protein.
thale cress.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ittel, M.E., Garnier, J.M., Jelisch, J.M. and Newerysury. Chicken poly(Abp-ribose) synthetase: complete deduced amino acid chicken poly(Abp-ribose) synthetase: complete deduced amino acid sequence and comparison with mammalian enzyme sequences sequence comparison with mammalian enzyme sequences dene 102 (2), 157-164 (1991)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1806 GATTATAACGCGGGATAATCTACCCCGGGAAAGCTAAGCACAAAAGGTGTGGGGAAAACA 1865
                                                                                                                                                                                                                                                                                                                    1746 GATGGCGTTCTGCTCTCTGCGGGGTTCCTTTGGGAGACATGAACTTCTGTATTCA 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 ccggtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaac 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (30-MAY-1990) Ittel M.-E., Centre de Neurochimie du
C.N.R.S., 5 Rue Blaise Pascal, 67084 Strasbourg Cedex, France
2 (bases 1 to 3036)
                                                                                                                                                                                                                                             1626 GGTCTGCGAATAGCTCCTCTGAAGCGCCTGTAAACTGGTTACATGTTTGGAAAAGGGGTT 1685
                                                                                                                                                                                                                                                                                                                                                               298 gigccaciggagicagagittgigaagiggagggatgatgicgiagitccctgcgggcaag 357
                                                                                                                                                                                 1566 AACAGGATGCTACTCTGGCACGGTTCACGTCTCACTAACTGGGCTGGTATTTTATCTCAA 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                    238 gccacgtccatggacaaacctccaagaggaagcattcgaccaagggattaggcaaaacc 297
                                                                                                                                                                                                                  61 gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                                                                                                                                                                                                                         121 tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-1993
                                                                                                                                              1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60
                                                                                                               3; Gaps
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Chicken mRNA for poly(ADP-ribose) polymerase (EC 2.4.2.30).
X52690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 acatcccaggtgaagatgcagttcttgctgaaggtgcgtttccatcacaagaggta 473
                                                                         Score 154.4; DB 8; Length 2147; Pred. No. 1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Data kindly reviewed (27-AUG-1990) by Niedergang C.
                                                                                                               0; Mismatches 191; Indels
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al Similarity 59.2%;
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/codon_start=1
/protein_id="CAA36917.1"
/db_xref="G1:63743"
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                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3845)
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalonebcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny,D.M., Glbbs,R.A.
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PHDFCMKRPPLLNNADSVOAKVEMLDNLLDIEVAYSLLRGGSDDSSKDPIDVNYEKLK
TDIKVVDRDSEEAEVIRKYVKNYHATTHNAYDLEVIDIEKIERGESORYKPFROLHN
                                                                                                                Submitted (30-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AWHSKNFTKYPKKFYPLEIDYGQDEEAVKKLTVKPGTKSKLPKPVQELVGMIFDVESM
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TGIPSGVNDTCLLYNEYIVYDIAQVNIKYLLKLKFNFKTSLW"
930 c 1080 g 793 t
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                                                                                                                                                                                                                 Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                              Strausberg, R.
      Mus musculus
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3; Gaps

DB 10; Length 3845;

Best Local Similarity 59.39 Matches 278; Conservative

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Embryophyta; Tracheophyta;
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AKARGVAANGGKKDVIQRLLSATAGPAAVADGGPLGAKEVIKGGDEEVEVKKEKNYTA
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SFMVYNRWGRVGVRGQDKLHGFSPTRDQAIYEFBGKFHNKTNNHWSDRKNFKCYAKKY
2625 AACCGGAGGCTGTGGCACGCTCCAGGACCACCAACTTTGCTGCCATGTCGTGGCAG 2684
                                                                                                                       2685 Gercreccaraccreaecrecreses 2744
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                                                                                                                                                                                                                                                                                                                                                                                    241 acgtecatggacaaacetecaagagggaagcattegaceaagggattaggeaaaacegtg 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ccactggagtccagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 gigocalcalcaatlaggagctotgaactcaigtacaatgaggagtacalcglotacaacaca 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 2295)
Babylchuk, E., Cottrill, P., Storozhenko, S., Fuangthong, M., O'Farrell, M., Van Montagu, M., Inze, D. and Kushnir, S.
Higher plants possess two poly(ADP-ribose) polymerases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZMPARPI 2295 bp mRNA
Zea mays mRNA for poly(ADP-ribose) polymerase (2295bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3042 GCTCAGGTGAATCTCAAATACCTGCTGAAACTCAAGTTCAATTTAAAGA 3090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-NOV-1997) Kushnir S., VIB, Dep.Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 teccaggigaagaigeagitetigeigaaggigegitteeateaeaaa 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="secondary protein modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="poly(ADP-ribose) polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ledeganckstraat 35, Gent, B9000, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARP gene; poly(ADP-ribose) polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:050017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA10888.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="2ea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:2959360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ222588.1 GI:2959359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="PARP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 2295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="PARP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2068
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Evers,R., Hammer,A. and Cornelissen,A.W.C.A.
Unusual C-terminal domain of the largest subunit of RNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3172)
                                                 SMIKSYLRNTHGKTHSGYTVDIVOIFFVSRHGETERFOKFASTRNRHLJAHGSKLSNN
AGILSGGLRAPPEARVTGYGYMGKGVYFADMFSKSANYCYASEACRSGVLLLCEVALG
DMNELLNADYDANNIFFKRIBSKGVQCJAPNNVESKVADDGVVVPLGEPKQEPSKRGG
LLYNBYLYNVDQIRMRYVLHVNFNRFRR"
TWLEMDYGETEKEIEKGSITDQIKETKLETRIAQFISLICNISMMKQRNVEIGYNAEK
LPLGKLRKATILKGYHVLKRISDVISKADRRHLEQLTGEEYTVIPHDFGFRKMREFII
DYPQKLKAKLEMVEALGEIEIATKLLEDDSSDQDDFLYARYKQLHCDFTPLEADSDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding protein; NAD(+) ADP-ribosyltransferase; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1949 CCCAAACAGGAACCTTCCAAAAGGGGTGGCTTGCTTTATAATGAGTACATAGTGTACAAC 2008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1889 GCACCTAACATGGTCGAGGTCGCTGACGATGGTGTTGTTGTTCCCCTTGGCGGAA 1948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 ccggtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaac 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1709 racitiscisacarstricaaasassesaactarisciacscrisaassatstasa 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 acgrecatgg---acaaacetecaagagggaagcattegaceaagggattaggeaaaace 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 gtgccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaag 357
                                                                                                                                                                                                                                                                                                       121 tacttigcagatctagtaagcaagagcacaatactgttatgtggataggaataatcct 180
                                                                                                                                                                                                                                                                                                                                                     61 gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submitted (26-JAN-1989) Huppi K., NCI/NIH, Lab of Genetics, Submitted (26-JAN-1989) Huppi K., NCI/NIH, Lab of Genetics, Submitted (26-JAN-1989) Huppi K., NCI/NIH, Lab of Genetics, 20 (bases 1 to 3172)
                                                                                                                                                                                                                                                                               1 aacaagaigciattaiggcaeggiicaaggiigaegaaiitigigggaaiicitagicaa 60
                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2009 GTAGACCAGATAAGAATGCGGTATGTCTTACATGTTAACTTCAATTTCAAGAG 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     418 acatcccaggtgaagatgcagttcttgctgaaggtgcgtttccatcacaagag 470
                                                                                                                                                                                                         y Match 31.9%; Score 151.4; DB 8; Length 2295; Local Similarity 59.0%; Pred. No. 9.3e-37; nes 279; Conservative 0; Mismatches 191; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
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                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                 ORIGIN
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g δλ q ò

g Qγ

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q ŏ Nucleic Acids Res. 17, 3387-3401 (1989) Location/Qualifiers /organism="Mus musculus"

source JOURNAL

II of Chithidia fasciculata

TITLE

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WISKNETKY PKKEY PLEIDYGODEBENYK LIVK PGTK SKLP KPYOELVGHIF DYDSMK
WISKNETKY PKKEY PLEIDYGODEBENYK LIVK PGTK SKLP KPYOELVGHIF DYDSMK
KALVEY ELDLOKMPLGKLSRRQI ODAAK SILSEVOGPY SGGSSESQI LDLSNRFYTLIP
PDPGMKK PPLLUNDASVOAK VEMLONILD EVAY SELLRGGSDSSKDP DIVNY PEKLKT
BDIK VVDRDS EBENEY IRKY VKNYHATTHIMA PLIEV IDIFK I BREGESGRYK RF FROLHN
TGLIMLGEV ALGORIK ELKHASHI SKLPRGK SKGLGKTTPDPSASITLEGVEVPLGT
IGLIMLGEV ALGORIK ELKHASHI SKLPRGK SKGLGKTTPDPSASITLEGVEVPLGT
GIPSGVNNTALLY NBY I VYDIAQYNK YLLKLK KFNFKTSLM"
                                                                                                                                                                                                                                                                                                                                             TPKEFREISYLKKLKYKKODRIFPPESSAPTTVHWPLSVTSAPTAVNSSAPADKPLSN
MKITLGKLSONNDEAKAVIEKLGGRLTGSANKASLGISIKKEVEKMNKKMEEVKEAN
NKITLGKLSONNDEAKAVIEKLGGRLTGSANKASLGISIKKEVEKMNKKMEEVKEAN
IRVJSEDFLODVSASTYSLQDLLSAHSLSPMGAEVKAEPGEVVAPRKKRAAPSKKSKG
KEREGVNKSEKRMLTILKGGAAVDPDSGLEHSAHVLEKGGKVFSATIGIVDIVKGTN
CFKEBGVNKSEKRMLTILKGGAAVDPSGLEHSAHVLEKGGKVFSATIGIVDIVKGTN
MYNTOLLONDENSENTWHFRSWGRLGTVIGSIKLLEOMPSKERAVEOPMKLYEEKTGNA
                                                                                                                                                                                                              /translation="maeaserlynoyyaksgrasckkcsesipkdslrmaimvospmpdgkvphyyhesgrundgkgddgs

dgkvphyyhythsgrwkydgtrhpdveydgfselrmddgkyyhytheggdgs

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toevakrddefaperaasolkgfsllsaedkealkkglpathvegkrkddeydgdbe

vakrksreddfysklekalkrdnellindydfydgybgdb

saildpradmargalleckerggglyfkrsdhyygtgdytawyrgnprygwysgy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2887 TCACATÀTCAGCAAGTTACCCAAGGCAAGCACAGTGTCAAAGGTTTGGGAAAAAC--- 2943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2944 ACCCCTGACCCTTCGGCCAGCATCACCCTGGAGGGTGTAGAGGTTCCACTGGGAACAGGG 3003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2767 racitricccacargererccaaagrecaaacracacacacacarcreaggagacce 2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 gigocatcatcaattaggagcictgaactcaigtacaatgagtacatcgictacaacaca 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 ccactggagtcagagtttgtgaagtggaagggatgatgatgtcgtagttcctgcggcaagccg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2707 ĠĠŦĊŦĠĊĠĠĸĬĸĠĊĊĊĸĸĊĊĬĠĸĸĠĊĠĊĊĠŶĠĸĸĠĠĠĊĬĸĊĸĬĠŦŶŦĠĠĠĸĸĸĠĠĸĸĊ 2766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2647 AACCGGAGGCTGTGGGACGGCTCCAGGACCACCAACTTGCTGGCATCCTGTGCAG 2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 tactttgcagatctagtaagcaaagagcgcacaatactgttatgtggataggaataatcct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60
                                                                                      /note="poly (ADP-ribose) polymerase (AA 1 - 1013)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.8%; Score 150.6; DB 10; Length 3172; 59.1%; Pred. No. 1.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2743. .2823
/note="DNA-binding domain A"
2898. .2952
                                   /tissue_type="spleen"
/clone="pADP3-2.1 and pADP-3C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2898. 2952
/note="DNA-binding domain B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="zinc finger domains"
                                                                                                                                                                                                           /db_xref="SWISS-PROT:P11103"
                                                                                                                                             /protein_id="CAA32421.1"
/db_xref="GI:49894"
                                                                                                                                                                                        xref="MGD:MGI:87933"
              /db_xref="taxon:10090"
/strain="BXSB"
                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                779 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 277; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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3064 GCTCAGGTGAATCTCAAATACCTGCTGAAACTCAAGTTCAATTTTAAGA 3112

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YHPKCFVQKREELGFRPEFSATHLMGFSVLTAEDQFTLKKOLLAIKGERKRKGDEVDG
IDEVTKKKSKKEKDKEIKLEKALRAQNDLINNVDELKRACSTNDLKELLFINKGEVD
SGESALLDFNVADGMVFGALLPCEECSGQLVFKGDAYYCDTAWTKCMYTQTPNRK
BWYTPKEFREISYFKKLKIKKODRIPPESSTPVGAAAPPSAASAPAAVHGCPDRRK
SNMKILTLGKLSQNFNEVRATIEKLGGKLTGTANKASLCISTKKFVDKLKKKMEEVKE
                                                                                                                                                                                                                                                                                                                                                                    Cloning of a full-length cDNA encoding bovine thymus poly(ADP-ribose) synthetase: evolutionally conserved segments and their potential functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zinc-binding finger motifs are observed in seq. 21-51 and 128-165.
The sequences, 200-220 and 250-270, showed helix-turn-helix structure. Nucleotide-binding fold was found in seq. 890-903.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /traislation="maessbklyrveyaksgrasckkckestpkdstrmarmvespmp
DGKIPHWYHLSCFRWVGFSIWHPDVEVEGFSELRWDDQOTIKRAAETGGRTDVSGKGQ
DGVGSKTERTLIDFGAGYAKSNRSTCKSCMEKIDKGQVRLSKKVYYPDRFQLGWVDCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Clinical Science and Laboratory Medicine Faculty of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTNSTYRLOLLEDDKESRYWIFRSWGRYGTYJGSNKLEDWPSKEDAIEHFWKLYEEKT
GNAWHSKNFTKHPKKFYPLEIDYGQDEEAVKKLTVNPGTKSKLFKPVQNLIKMIFDVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANIRVVSEDFLQDISASTKSLQELLSTHLLSPWGAEVKVEPVEAVGPKGKSGAAPSKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKGPVKEBGTNKSEKRMKLTLKGGAAVDPDSGLEHNAHVLEKGGKVFSATLGLVDIVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMKKANVEYEIDLOKMPLGKLSKROTOAAYSILSEVQQALSQGSSDSHILDLSNRFYT
LIPHDFGMKKPPLLNNANSVQAKVEMLDNLLDIEVAYSLLRGGSDDSSKDPIDVNYEK
LKTDIKVVDKDSEEAEIIRKYYKNTHATTHNAYDLEVVDIFKIEREGESQRYKPFKOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNRRLLWHGSRTANFAGILSQGLRIAPPEAPYTGYNFGKGIYFADMVSKSANYCHTSQ
GDPIGLILLGEAALGNNYELKHARHISKLPKGKHSVKGLGKTTPDPSASITVDGVEVP
                                                                                                                                          DNA binding protein; helix-turn-helix; nuclear location signal; poly(ADP-ribose) synthetase; zinc-binding finger motif.

Bovine thymus, cDNA to mRNA, clone pso-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             These data kindly submitted in computer readable form by: Isao
                                                                               07-FEB-1999
                                                                                                                                                                                                                                                                                                      1 (bases 1 to 3389)
Salto,I., Hatakeyama,K., Kido,T., Ohkubo,H., Nakanishi,S. and
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                                                 BOVPAS 3589 bp mRNA MAM 07-FF
Bovine poly(ADP-ribose) synthetase (EC 2.4.2.30) mRNA.
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/note="nuclear location signal"
1010 q 725 t
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Shogoinkawahara-cho 54, Sakyo-ku
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/db_xref="GI:217582"
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77. .3127
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075-771-4792
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Salimann,F.R., Vodenicharov,M.D., Wang,Z.O. and Poirier,G.G. Characterization of saRp-1. An alternative product of PARP-1 gene with poly(ADP-ribose) polymerase activity independent of DNA strand
2648 AACCGGAGGCTGCTGGCACGGGTCCAGGACCACCAACTTCGCGGGCATCCTGTCCCAG 2707
                                                   2828 ATAGGCTTGATCCTGTTGGGAGAGCTGCCCTTGGAACATGTATGAACTTGAACATGCT 2887
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                                                                                                                        121 tactitigcagatctagtaagcaagagcgcacaatactgitatgtgggataggaataatcct 180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1732)
                                                                                                                                                                                           181 gtaggitigatgetietitetgaggitigetitaggagaeatgiatgaactaaagaaagee 240
                                                                                                                                                                                                                                                                                                                                                                2945 ACCCCTGACCCATCGGCTAGTATTACTGTGGATGGTGGAGGTGCCTCTCGGGACAGGG 3004
                                                                                                                                                                                                                                                              241 acgiccaiggacaaacticcaagaggaagcaitcgaccaagggaitaggcaaaaccgig 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1732)
Sallmann,F.R., Vodenicharov,M.D., Wang,Z.-Q. and Poirier,G.G.
Direct Submission
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/db_xref="taxon:10090"
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/db_xref="G1:7363322"
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/dev_stage="embryo"
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Cricetulus griseus poly ADP-ribose polymerase (PARP) mRNA, complete
                                                              RRLLWHGSRTTNFAGILGOGLRIAPPBAPVTGYMFGKGIYFADMVSKSANYCHTSQGD
PIGLIMLGEVALGNMYELKHASHISKLPRGKHSVKGLGKTTPDPSASITLEGVEVPLG
TGIPSGVNDTCLLYNEYIVYDIAQVNLKYLLKLKFNFKTSLW"
                                                                                                                                                                                                                                                                                       ;
KKALVEYEIDLQKMPLGKLSRRQIQAAYSILSEVQEPVSQGSSESQILDLSNRFYTLI
                    PHDFGMKKPPLLNNADSVLAKVEMLDNLLDIEVAYSLLRGGSDDSSKDPIDVNYEKLK
                                         TDIKVVDRDSEEAEVIRKYVKNTHATTHNAYDLEVIDIFKIEREGESQRYKPFRQLHN
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Submitted (14-701-1999) Oncological Sciences, University of Utah,
15 N. 2030 E., Salt Lake City, UT 84112, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg
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Pred. No. 5.1e-36;
0; Mismatches 190; Indels
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Similarity 58.8%;
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FEATURES

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DGKYPHWYHESCHWUGHSTROPDUEVDGFSELRUMDDQKVKKTAEAGGVAGKGODGS
DGKSERTLGDFAAEYAKSNRSTCKGCMEKIEKGQVRLSKKMLDPEKPQLGMIDRWYHP
TCFVKRREELGFRPEXSQLAGGSELLSABDKEULKROLPGWAEGERKGGEVDGADE
TCFVKRREELGFRPEXSQLAGGSELLSABDKEULKROLPGWAEGERKGGEVDGADE
VAKKXSKGKDKDSKLERALKAQNDLIWNIKDELKRACSTSDLKELLIFNOQOVPSGE
SALLDRVADGHARGALLDFCKECSGQLVFKSDAYYCTGDVTAWTKCMVKTQTFSRKEWY
TPKEPREISTYLKKIVKKQDRIFPPETSAPAPPHLPEYSTAAPPANSSCPANKFLSN
MKILTLGKLSQSKDEARATIEKLGGKLTGSANNSSLCISTKREVEKMCKWEBYQAAN
VRVVCEDFLODVAASTKSLOELLSAHSLSSNGARAVKREVENGKKMEBYQAAN
SYYKLQLLEDDRESRYWIFRSNGARYGYTGSNLLQDWBSKEDAVBHFMKLYEBKGTN
WHSKNFTKYPKKYPLLNGGAAVDPDSGLEHSAHVLEKGGRVESATLGLYDTWGTN
WHSKNFTKYPKKYPLLNGGAAYSTLTSTYNGAAYSTLIP
KALVEYEDIOLQKWPLGKLSKRQIQAAYSILSEVQAVVBEKKKT
HDFGNKKPPLLNANDSVQAKVBRIDNILDIFLSHYXSLLEGGSDSSKDPTDWYBKLKT
HDFGNKKPPLLNANDSVQAKVBRIDNILDIFLSHYXSLLEGGSDSSKDPTDWYBKLKT
HDFGNKYRPLLNANDSVQAKVBRIDNILDIFLSHYXSLLEGGSDSSKDPTDWYBKLKT
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IGLILLGEVALGNMYELKHASHISKLPKGKHSVKGLGKTTPDPSASITLEGVEVPLGT
GIPSGVNDTCLLYNEYIVYDIAQVNLKYLLKLKFNFKTSLM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                         /protein_id="AaD45817.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIKVVDRDSEEAEVIRKYVKNTHATTHNAYDLEVMDIFKIEREGESQRYKPFKQLHNR
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                                                                                                                                                                                                                                                                  /product="poly ADP-ribose polymerase'
                 /organism="Cricetulus griseus"
/db_xref="taxon:10029"
/cell_line="V79-4"
                                                                                                                                                                                                            /EC_number="2.4.2.30"
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                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                              /gene="PARP"
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Matches 27
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Search completed: March 7, 2002, 16:49:01 Job time: 8171 sec

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AAX89542
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1362.065 Million cell updates/sec
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                                                                                                                                          March 7, 2002, 18:16:17; Search time 298.35 Seconds
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/SIDS2/gcgdata/geneseq/yeneseqn/NA1984.DAT:*
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/SIDS2/gcgdata/geneseq/yeneseqn/NA1989.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                 930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC Gapor 10.0 Gapor 1.0
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:*

			Description	Maize poly ADP-rib	DNA encoding the p	Human poly(ADP-rib	DNA-binding domain	Human tankyrase2 r	5.3 kb EcoRI fragm	Poly(ADP-ribose)-p	3' end fragment of			
SUMMARIES			TD		AAZ60615	AAZ60618	AAZ60617	AAZ60616	AAZ23799	AAT13732	AAF63954	AAT04221	AAT04219	AAC85320
			198	20	21	21	21	21	20	17	22	16	16	22
		Query	Length	2949	3211	3212	2147	2295	3580	3793	3045	5345	2682	864
,	æ	Query	Match	100.0	100.0	100.0	32.6	31.9	30.1	30.1	29.4	29.1	28.7	25.9
		ć	score	474	474	474	154.4	151.4	142.6	142.6	139.4	137.8	136.2	122.6
		Result		1	7	m	4	S	9	7	80	6	. 10	11

Human poly(ADP-rib	nparps cona. Homo	Human brain PARP2	Human brain poly-A	Human ORFX ORF2673	Fusion protein PAR	Human cDNA sequenc	Human colon cancer	Poly(ADP-ribose)-p	Enterococcus faeca	Human brain PARP3		Probe #9163 used t	NAD(+) ADP-ribosyl	EST AA568817, frag	Colon tumour relat	H. Pylori GHPO 150	Human cDNA clone (Human secreted pro	Aspergillus oryzae	Codon-optimised mu	Shrimp white spot	Human cervical can	Arabidopsis thalia	ACNPV ORF 54, resi	Drosophila morphog	Drosophila morphog	Drosophila morphog	ACNPV genomic DNA	Human gene signatu	Human secreted pro	Human secreted pro	rsed H	Stromelysin gene c
AAF59996									AAX13509	AAZ44288							AAH12716						-	-		-			AAT24362		AAC0894	AAF7541	AAQ24140
22	77	21	22	21	22	22	21	16	20	21	21	22	15	22	22	19	22	21	21	22	22	22	21	17	19	20	21	17	16	21	21	22	13
1566	1814	1843	1843	1912	3200	1980	595	1592	3807	2265	2265	599	198	472	382	1406	296	1966	677		305107	441	527	1098	2625	2625	2625	133894	354	283	361	131	1160
25.9								23.0	7.9	7.4	7.4	7.1	7.0	7.0	7.0	6.9	6.8	6.7	6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.3	6.3	6.3	6.3
122.6										35	35		33.4		33	32.8	32.4	31.8	31	31	31	30.8	30.6	30.4	30.4	30.4	30.4	30.4		30	30	29.8	e,
175	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5
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ALIGNMENTS

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PARP; poly ADP-ribose polymerase; metabolism; maize; transform; ss.
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aa:Xaa)
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(pos:1495..1497, aa:Xaa)
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/transl_except= (pos:2011..2013,
/transl_except= (pos:2014..2016,
/transl_except= (pos:2056..2028,
/transl_except= (pos:2050..2049,
/transl_except= (pos:2050..2049,
                                                                                                                                                                                           Maize poly ADP-ribose polymerase gene
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..2949
/*tag= a
AAX89542 standard; cDNA; 2949 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "PARP"
                                                                                                                           (first entry)
                                                                                                                           06-0CT-1999
                                                               AAX89542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is the maize poly ADP-ribose polymerase (PARP) gene. The sequence codes a PARP with 982 amino acids (AAY28464). PARP is required in the cell in most cases of DNA repair, recombination, rearrangement and transposition. PARP gene and antisense gene can be used to transform plant cells and alter the metabolic state of the transformed cell. This is useful in enhancing disease resistance in plants and methods of genetic transformation of plants. Plants transformed with either a sense or antisense PARP nucleotide sequence may be utilized to increase transformation frequency in plant cells. The enzyme also plays a role in pathogen attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2476 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 2535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New maize poly ADP-ribose polymerase gene useful in transforming plants to alter their metabolic state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 474; DB 20; Length 2949; 100.0%; Pred. No. 1.3e-148; ive 0; Mismatches 0; Indels 0;
                                                                                                           aa:Xaa)
aa:Xaa)
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                /transl_except= (pos:2056..2059, as /transl_except= (pos:2077..2079, as /transl_except= (pos:21077..2109, as /transl_except= (pos:2107..2109, as /transl_except= (pos:2116..2118, as /transl_except= (pos:2119..2121, as /transl_except= (pos:2122..2124, as /transl_except= (pos:2122..2124, as /transl_except= (pos:2128..2124, as /transl_except= (pos:2128..2137, as /transl_except= (pos:2128..2137, as /transl_except= (pos:2128..2137, as /tote= "Xaa = unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 30-35; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (PION-) PIONEER HI-BRED INT INC.
  /transl_except=
                                                                                                                                                                                                                                                                                                                                                        99WO-US01591.
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Best Local Similarity 100.
Matches 474; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-444613/37.
P-PSDB; AAY28464.
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                                                                                                                                                                                                                                                                WO9937789-A1
                                                                                                                                                                                                                                                                                                                                                        26-JAN-1999;
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The present sequence encodes the ZAP1 protein of Zea.mays. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The ZAP1 polymucleotide sequences can be used for modulation of programmed cell death in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous ZAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation claimts that are resistant to fungior nematodes; are male or female sterile, or have better seed-shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or
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2776 ccactggagtcagagtttgtgaagtggagggatgatgttgttagttccctgcggcaagccg 2835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZAP1; poly(ADP-ribose) polymerase, PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding the poly(ADP-ribose) polymerase ZAP1 protein of Zea mays.
                                                                           gtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacaca
                                                                                                           2836 gtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacaca
                                                                                                                                                                                                                           /product= "2AP1 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ60615 standard; DNA; 3211
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P-PSDB; AAY68833.
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                                                                       361
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Sequence 3211 BP; 968 A; 604 C; 813 G; 826 T; 0 other;

complete plants).

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                                                                                                                                                                                                                                      ZAP2; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter; ss.
                                                                                                                                  2849 ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcgggcaagccg 2908
                                                        2549 aacaagatgctattatggcacggttcaaggttgacgaattttgtggggaattcttagtcaa 2608
                                                                                                              2609 gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 2668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding the poly(ADP-ribose) polymerase ZAP2 protein of Zea mays.
                                                                                       gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                                                                                                                                                                                                      ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg 360
                                                                                                                                                                                                                                                                                                                  361 gigocatcatcaattaggagetetgaacteatgiacaatgagiacategtetacaacaea 420
                                                                                                                                                                                                                          241 acgtccatggacaaacctccaagagggaagcattcgaccaagggattaggcaaaaccgtg 300
                      Gaps
                                            1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60
                                                                                                                                                                                                                                                                                                                             0;
Length 3211;
                      Indels
100.0%; Score 474; DB 21;
100.0%; Pred. No. 1.3e-148;
ive 0; Mismatches 0;
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/product= "ZAP2 protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                       Matches 474; Conservative
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            Similarity
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  Query Match
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The present sequence encodes the ZAP2 protein of Zea mays. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The ZAP2 polymucleotide sequences can be used for modulation of programmed cell death in plants, to induce, or protect against, programmed sell death, in plants, to induce, or protect against, programmed cell death, of which parp activity is reduced. Reducing expression of endogenous ZAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, of stress (cold, chemical treatments, pathogens, pests, drought, heat, cor during transformation). Particular applications are generation of plants that are resistant to fungion nematodes; are male or female sterile, or have better seed-shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or
Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 474; DB 21; Length 3212; 100.0%; Pred. No. 1.3e-148; Live 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3212 BP; 974 A; 600 C; 815 G; 823 T; 0 other;
                                                                   Disclosure; Page 103-108; 126pp; English.
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Matches 474; Conservative
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TD AAZ66617
XX AAC AAZ6C
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The present sequence encodes a NAP protein. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polynucleotide sequences can be used for modulation of programmed cell death in eukaryotic cells. The method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to induce, to increase growth rate and to produce plant cells that are more tolerant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
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NAP: poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter; ss.
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                                                                                                                                                                                                                                                                                                                                                                    /product- "NAP protein"
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                                                                                                                                                                                                                                           Location/Qualifiers
129..2042
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                                                                                                                                                               Arabidopsis thaliana.
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P-PSDB; AAY68835.
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                                                                                                                                  1566 aacaggatgctactctggcacggttcacgtctcactaactgggctggtattttatctcaa 1625
                                                                                                                                                                                                   1686 tactttgcggatatgttctccaagagtgcgaactattgctatgccaacactggcgctaat 1745
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                                                Gaps
                                                                                        1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60
Score 154.4; DB 21; Length 2147; Pred. No. 2.1e-41; 0; Mismatches 191; Indels 3;
  32.68;
59.28;
                                         282; Conservative
                    Similarity
  Query Match
Best Local §
                                       Matches
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The present sequence encodes the NAP protein of Zea mays. This protein lis a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polynucleotide sequences can be used for modulation of programmed cell death in eukaryotic cells. The method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant

Example 1; Page 89-92; 126pp; English.

of stress (cond, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation of plants that are resistant to fungi or nematodes; are male or female sterile; or have better seed shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or

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Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
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                                                                                                                                                              1866 gcaccaaacccatcagaggctcaaacactagaagacggtgttgttgttccacttggcaaa 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter; ss.
                                                                                              gtgccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaag 357
                                                                                                                                                                                                                             coggigocatcatcaattaggagcictgaactcatgiacaatgagiacatcgictacaac 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding the poly(ADP-ribose) polymerase NAP protein of Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                      1986 giggaacaaatcaagaigcgitaigigatccaagicaaaitcaactacaagcacta 2041
                                                                                                                                                                                                                                                                                                                                                          418 acatcccaggtgaagatgcagttcttgctgaaggtgcgtttccatcacaagaggta 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "NAP protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ60616 standard; DNA; 2295 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
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                                                                                                                                                  1589 aataggatgettttgtggeatggtteteggttgageaaetgggetgggateettteteag 1648
                                                                                                                                                                                               1709 tactitigctgacatgitticaaagagigcaaactatigciacgccictgaagcaigiaga 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                           1889 gcacctaacatggtcgagtctaaggtcgctgacgatggtgttgttgttccccttggcgaa 1948
                                                                                                                                                                                                                                                                                                                           gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggctc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                gigocaciggagicagagittgigaagiggagggatgatgicgiagitcccigcggcaag 357
                                                                                              Gaps
                                                                                                                           1 aacaagatgctattatggcacggttcaaggttgacgaattttgtggggaattcttagtcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct
                                                                                                                                                                                                                                                                                                 241 acgtccatgg---acaaacctccaagagggaagcattcgaccaagggattaggcaaaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coggtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaac
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                                                                  Length 2295;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 acatcccaggtgaagatgcagttcttgctgaaggtgcgtttccatcacaagag 470
                                                                 Score 151.4; DB 21; Length
Pred. No. 2.2e-40;
0; Mismatches 191; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "poly(ADP-ribose) polymerase"
                       G; 583 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human poly(ADP-ribose)polymerase cDNA.
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                         Sequence 2295 BP; 668 A; 447 C; 597
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140..3184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ23799 standard; cDNA; 3580
                                                                 Query Match 31.9%;
Best Local Similarity 59.0%;
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98DE-1008889
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complete plants)
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This invention describes a novel vector (A), suitable for gene therapy, which contains a DNA insert (I) that encodes a practically complete poly(adenosine diphosphate-ribose) polymerase (PARP) which has antitumor activity. PARP is a nuclear DNA repair enzyme (activated by strand breakage), that allows recovery of proliferating cells from the toxic effects of DNA damage (caused by alkylating or oxidizing agents or radiation), and protects cells against such damage or other causes of genomic instability. (A) are used for treatment of cancer and for cancer prevention in subjects at high risk (e.g. those with tumor-associated genetic defects). Thus cells treated with (A) show an increased tendency to die when treated with radiation or chemotherapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                   agent, and in cells that survive this treatment they inhibit genomic instability, so should reduce the likelihood of further development of both malignant cells and resistance to chemotherapy. This sequence encodes the human poly(ADP-ribose) polymerase described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3062 atttcatctggtggaatgacacctctctactatataacgagtacattgtctatgatatt 3121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2705 aaccgaagattgctgtgggcacgggtccaggaccaccaactttgctgggatcctgtcccag 2764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3005 cctgatccttcag---ctaacattagtctggatggtgtagacgttcctcttgggaccggg
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                                                                                                     poly(adenosine
treating or preventing tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 30.1%; Score 142.6; DB 20; Length Best Local Similarity 58.0%; Pred. No. 2.4e-37; Matches 272; Conservative 0; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3580 BP; 986 A; 823 C; 996 G; 775 T; 0 other;
                                                                                                     New gene therapy vector expressing diphosphate-ribose)-polymerase for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT13732 standard; DNA; 3793
                                                                                                                                                                  Claim 4; Fig 1; 12pp; German.
Buerkle A, Meyer R;
                                     WPI; 1999-509563/43.
                                                           P-PSDB; AAY33699
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(first entry)

31-OCT-1996

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The present sequence encodes a poly(ADP-ribose) polymerase (PARP) contg. a DNA-binding domain (DBD). The DNA fragment from -29 to + 1127 (nucleotides 67-1220 of this sequence) encoding the DBD can be inserted into vectors which are used for gene therapy. Over-expression of the DBD inhibits the DNA repair function of PARP, so the vectors are useful for gene therapy or tumours, esp. in combination with conventional chemo-
                                      PARP; DNA-binding domain; poly(ADP-ribose) polymerase; gene therapy;
            domain of poly(ADP-ribose) polymerase coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Vectors contg. insert encoding DNA-binding domain of poly(ADP-ribose) polymerase · useful for gene therapy, esp.
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                                                                                                                                              /product= poly(ADP-ribose)_polymerase
/note= "PARP"
                                                                                                                                                                                                      /note= "encodes DNA-binding domain"
                                                     tumour treatment; DNA repair; over-expression; ss.
                                                                                                                                                                                                                                                                                                                                               (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                          Location/Qualifiers
96..3137
                                                                                                                                                                                                                                                                                                                                                                          Buerkle A, Kuepper J, Zur Hausen H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            poly(ADP-ribose) polymerase
tumours
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                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                         15-DEC-1995;
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              DNA-binding
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                                                                                                                          gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                                                                                                                      tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct 180
                                                                                                                                                                                                                                                 gtaggtttgatgcttctttctgaggttgctttaggagacatgtatgaactaaagaca 240
                                                                                                                                                                                                                                                                                                                300
                                                              1 aacaagatgctattatggcacggttcaaggttgacgaattttgtggggaattcttagtcaa 60
                                                                                                                                                                                                                                                                                                           241 acgtccatggacaaacctccaagaggaagcattcgaccaagggattaggcaaaaccgtg
                                                                                                                                                                                                      30.1%; Score 142.6; DB 17; Length 3793; 58.0%; Pred. No. 2.5e-37;
                                 3;
                                194; Indels
                              0; Mismatches
                                Conservative
              Similarity
                Local Simi
 Query Match
              Best Loca
Matches
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New tankyrase2 polypeptides, useful for treating conditions mediated by poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
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                                                                              301 ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 aacaagatgctattatggcacggttcaaggttgacgaattttgtggggaattcttagtcaa 60
                                                                                                                                                                                                                                                                                                                                                               Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
inflammatory disorder; ds.
                             2958 cctgatccttcag---ctaacattagtctggatggtgtagacgttcctcttgggaccggg
                                                              361 gtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3045;
                                                                                                                                              421 teccaggigaagaigeagiteitgeigaaggigegitteeateacaaga 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.4%; Score 139.4; DB 22; Length 57.6%; Pred. No. 2.7e-36; ive 0; Mismatches 196; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McElligott DL;
                                                                                                                                                                                                                                                                                                                                 Human tankyrase2 related coding sequence SEQ ID NO: 136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3045 BP; 863 A; 710 C; 851 G; 621 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldman PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 203-207; 242pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory and autoimmune disorders -
                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                    AAF63954 standard; DNA; 3045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Christenson E, Demaggio AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2000; 2000WO-US17827
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Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-102896/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ICOS-) ICOS CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JAN-2001
                                                                                                                                                                                                                                                                   AAF63954;
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                                                                                                                                                                                                                                                                                                                                                                 Human;
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31-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT04219;
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                                                                                                          121
                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                          361
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                                                                                                                                                                                                            2806 teacatateageaggttaececaagggeaageacagtgteaaaggtttgggeaaaaetaee 2865
241 acgtccatggacaaacctccaagaggaagcattcgaccaagggattaggcaaaaccgtg 300
                                                                                                                                                                                                361 gigocatcatcaattaggagcicigaacicaigtacaaigagtacatcgictacaacaca 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contains
                                                             5.3 kb EcoRI fragment containing poly(ADP-ribose)-polymerase gene
                                                 181 gtaggittgaigcitcittctgaggitgcittaggagacaigtaigaactaaagaaagcc
                                                                                                                                                                       2866 octgatoottcag---ctaacattagtctggatggtgtagacgttcotottgggaccggg
                                                                                                                                                  ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allele-specific primers for detecting pre-disposition to cancer caused by a deletion in chromosome 13 pseudo-gene for poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

29.1%; Score 137.8; DB 16; Length 5345;
Best Local Similarity 57.4%; Pred. No. 1.2e-35;
Matches 269; Conservative 0; Mismatches 197; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA primer; PCR: polymerase chain reaction;
polyADP-ribose)-polymerase; cancer diagnosis; chromosome-13;
pseudogene; Burkitt's lymphoma; B-follicular cell lymphoma;
small cell lung carcinoma; colorectal carcinoma; tumor;
                                                                                                                                                                                                                                                             This sequence corresponds to a 5.3 kb EcoRI fragment that
                                                                                                                                                                                                                                                421 teccaggigaagaigeagitetigeigaaggigegiiteeaieaeaaga 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5345 BP; 1598 A; 1142 C; 1396 G; 1209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the poly(ADP-ribose)-polymerase pseudogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 41-46; 47pp; English.
                                                                                                                                                                                                                                                                                                                                     AAT04221 standard; DNA; 5345 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smulson ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0044618.
88US-0257696.
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADP-ribose) polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cherney B, Lyn D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breast carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-1993;
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3819 cctgacctttcag---ctagtatcccactggatggtgtagaggttcctcttgggaccagg 3875
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                                                   3759 tcacatatcagcaagttacccaagggcaagcacagtgtcaaaggtttgggcaaaactact 3818
                                                                                                                               241 acgtccatggacaaacctccaagaggaagcattcgaccaagggattaggcaaaaccgtg 300
                                                                                                                                                                                                                                                                      ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcgggcaagccg 360
                                                                                                                                                                                                                                                                                                                            gtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacaca 420
aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa
                                                                                                           tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allele-specific primers for detecting pre-disposition to cancer caused by a deletion in chromosome 13 pseudo-gene for poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poly(ADP-ribose).polymerase alpha-allele DNA from chromosome-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      poly(ADP-ribose)-polymerase; cancer diagnosis; chromosome-13; pseudogene; Burkitt's lymphoma; B-follicular cell lymphoma; small cell lung carcinoma; colorectal carcinoma; tumor;
                                                                                                                                                                                                                                                                                                                                                                                                    421 tcccagtgaagatgcagttcttgctgaaggtgcgtttccatcacaaga 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer; PCR; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 31-36; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT04219 standard; DNA; 2682 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88US-0257696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caused by a deletion in (ADP-ribose) polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEOU ) UNIV GEORGETOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      breast carcinoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-327692/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lyn D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-OCT-1988;
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This sequence is of the poly(ADP-ribose).polymerase alpha-allele. A DNA primer specific to this sequence may be used in a PCR amplification method to differentiate between the alpha- and beta-
                                                                  alleles of the processed pseudogene.
22222×3
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Sequence 2682 BP; 772 A; 618 C; 711 G; 581 T; 0 other;

1;

2050 aactgaaggttgctgtggcatgggtccaggaccaacctttgctgggatcctgtcctg 2109 99tctttggatagccctgcctgaagcacctgtgatgggctacatgtttggtaaagtgatc 2169 2170 tatttcgctgatcttgtctccaagagtgccaacgactgccatacatcttaggaagacca 2229 2230 atagggttaatcctgtcggaagaagttgcccttggaaacgtgtggaactgaagcatgct 2289 2290 tcacatatcagcaagttacccaagggcaagcacagtgtcaaaggtttgggcaaaactact 2349 2350 cctgacctttcag---ctagtatcccactggatggtgtagaggttcctcttgggaccagg 2406 2407 gittcaiciggigigaatgacacigictacigitataaigagiacatigiciaigatati 2466 240 gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120 tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct 180 241 acgtccatggacaaacctccaagagggaagcattcgaccaagggattaggcaaaaccgtg 300 361 gigccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacaca 420 1 aacaagatgctattatggcacggttcaaggttgacgaattttgtggggaattcttagtcaa 60 301 ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg Score 136.2; DB 16; Length 2682; Pred. No. 3e-35; 0; Mismatches 198; Indels 3; 421 tcccaggtgaagatgcagttcttgctgaaggtgcgtttccatcacaaga 469 Query Match 28.7%; Best Local Similarity 57.1%; Matches 268; Conservative 2110 121 61 181 g ð ð g ò a ò g ò ΩD Op QQ ò ò g

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Human; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS; inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia; infarction; cerebral vasospasm; rheumatoid arthritis; osteoarthritis; goodylitis; Behcet's disease; sepsis; septic shock; endotoxic shock; gram negative sepsis; gram positive sepsis; trauma; toxic shock syndrome; multiple organ injury syndrome; vasculitis; hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy; eosinophilic granuloma; asthma; chronic bronchitis; allergic rhinitis;
                                                                                                                                                                                                                                                                                                                                                                                                                              chronic obstructive pulmonary disease; silicosis; reperfusion injury; pulmonary sarcoidosis; pleurisy; alveolitis; pneumonia; myocardium; bronchiectasis; pulmonary oxygen toxicity; keloid formation; brain; scar tissue formation; atherosclerosis; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune thyroiditis; multiple sclerosis; Reynaud's syndrome; graft versus host disease; allograft rejection; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chronic glomerulonephritis; inflammatory bowell disease;
Crohn's disease; ulcerative colitis; necrotizing enterocolitis;
inflammatory dermatosis; contact dermatitis; atopic dermatitis;
psoriasis; urticaria; fever; myalgia; meningitis; encephalitis;

 end fragment of hparp2, 3'-hPARP2.

                                           AAC85320 standard; cDNA; 864
                                                                                                                                              (first entry)
                                                                                                                                           29-MAR-2001
                                                                                             AAC85320;
11
                    AAC85320
RESULT
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Gaps

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Ω δλ

qq δλ

δ qq

1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60

Query Match 25.9%; Score 122.6; DB 22; Length 864; Best Local Similarity 56.9%; Pred. No. 6.2e-31; Matches 268; Conservative 0; Mismatches 194; Indels 9;

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New human poly(ADP-ribose) polymerase for treating inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (poly(ADP-ribose) polymerase) cDNA. This sequence was amplified using the primers given in AAC85315-17. DNA derived from a testis cDNA ilbrary was used as a template. The protein of the invention, bPARP2, causes the covalent addition of polymers of ADP-ribose to protein targets. hPARP2 activity is induced in many instances of oxidative stress or during inflammation where there is direct damage to the DNA. hPARP2 may be used to identify antagonists which may be used to treat a human having a disorder mediated by PARP2 activity, such as, inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders. hPARP2 and antibodies to it,
Sjogren's syndrome; alcoholic hepatitis; bacterial pneumonia; hypovolemic shock; Type I diabetes mellitus; hypersensitivity; leukocyte dyscrasia; thermal injury; cytokine-induced toxicity; expressed sequence tag; EST; RACE; PCR; amplify; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents the 3' fragment of the human parp2
                                                                                                                                                                                                                                                                                                                                                                                                                        Christenson E, Demaggio AJ, Goldman PS, McElligott DL;
                                                                                                                                                                                                      /product= "hPARP2 C-terminal fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 864 BP; 250 A; 207 C; 193 G; 214 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            can also be used to diagnose these conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 101; 129pp; English.
                                                                                                                                                     Location/Qualifiers
                                                                           polymerase chain reaction; ds.
                                                                                                                                                                                                                                                                                                              16-JUN-2000; 2000WO-US16629.
                                                                                                                                                                                                                                                                                                                                                  99US-0139543.
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                                                                                                                                                                                                                                          WO200077179-A2
                                                                                                                                                                                                                                                                                                                                                  16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metastasis
                                                                                                             Synthetic.
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This sequence represents cDNA encoding a novel human poly(ADP-ribose)
synthetase, sbhPARS2. The invention also relates to fragments,
variants and sequences with at least 95% identity to the sbhPARS2.

protein or nucleotide sequence; expression systems and host cells
comprising an sbhPARS2 nucleic acid sequence; the recombinant expression
of sbhPARS2; and an antibody specific for sbhPARS2. sbhPARS2 proteins
and nucleotides are useful as vaccines for inducing an immunological
response in a mammal. The sbhPARS2 protein is useful for identifying
compounds which inhibit or stimulate its activity or expression level.
Such agonists and antagonists of sbhPARS2 are useful for treating human
diseases including ischemial and ischaemic tissue injury (e.g., cerebral
and cardiac ischaemia, myocardial infarction, stroke), inflammation,
cutoimmune disease (e.g. diabetes, multiple sclerosis) and
neurodegenerative diseases (e.g., Parkinson's disease and Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human polypeptide of the polyADPribose synthetase family for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic assays and for screening modulators used for preventing and treating inflammation, autoimmune disease and Alzheimers disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "Human poly(ADP-ribose) synthetase sbhPARS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; poly(ADP-ribose) synthetase; sbhPARS2; vaccine; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkinson's disease; Alzheimer's disease; chromosome localisation; ss
                                                                                                                                                            736 agigacacaggaattotgaatocagatggitatacootcaactacaatgaatatigta 795
616 aatcctaaggccgaaggattgcttcaaggtaaacatagcaccaaggggctgggcaagatg 675
                                                                                                                    352 ggcaagccggtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtc 411
                                          298 gigocaciggagicagagitig----igaagiggagggatgaigtogiagitocoigc 351
                                                                                676 gctcccagttctgcccacttcgtcaccctgaatgggagtacagtgccattaggaccagca 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ischaemic disorder; cerebral ischaemia; cardiac ischaemia; myocardial infarction; stroke; inflammation; autoimmune disease; diabetes; multiple sclerosis; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhu Y;
                                                                                                                                                                                                                                             tataaccccaaccaggtccgtatgcggtaccttttaaaggttcagtttaat 846
                                                                                                                                                                                                         tacaacacatcccaggtgaagatgcagttcttgctgaaggtgcgtttccat
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                                                                                                                                                                                                                                                                                                                                                     AAF59996 standard; cDNA; 1566 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-AUG-2000; 2000WO-US21775.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Human; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS;
What inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia;
Inflammation; cerebral vasospasm; rheumatoid arthritis; osteoarthritis;
What infarction; cerebral vasospasm; rheumatoid arthritis; osteoarthritis;
What words shock; gram negative sepais; gram positive sepsis; rauma;
What toxic shock; gram negative sepais; gram positive sepsis; trauma;
What toxic shock syndrome; multiple organ injury syndrome; vasculitis;
Whenorrhage; conjunctivitis; uveatis; thyroid-associated ophthalmopathy;
Whonic obstructive pulmonary disease; silicosis; reperfusion injury;
Whonic obstructive pulmonary disease; silicosis; reperfusion injury;
Whonic obstructive pulmonary oxygen toxicity; keloid formation; brain;
Whonichiectasis; pulmonary oxygen toxicity; keloid formation; brain;
Who autoimmune thyroiditis; multiple sclerosis; systemic lupus erythematosus;
What versus host disease; allograft rejection; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                 5
disease). sbhPARS2 nucleic acids are useful as diagnostic reagents for detecting mutations in the associated gene; as hybridisation probes to isolate full-length sbhPARS2 cDNAs and sbhPARS2 genomic clones; and for chromosome localisation studies. The sbhPARS2 protein is also useful as an immunogen to produce antibodies for therapeutic use. sbhPARS2 proteins, nucleotides and antibodies are also useful in screening methods for detecting the effect of added compounds on the production of mRNA and
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                                                                                                                                                                                                                                                                                                                                   0; Mismatches 194; Indels
                                                                                                                                                                                                                 Sequence 1566 BP; 490 A; 328 C; 381 G; 367 T; 0 other;
                                                                                                                                                                                                                                                                                        25.9%; Score 122.6; DB 2 56.9%; Pred. No. 8.3e-31;
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                                                                                                                                                                                                                                                                                          Query Match 25.99
Best Local Similarity 56.99
Matches 268; Conservative
                                                                                                                                                                        protein in cells.
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WO200077179-A2. 21-DEC-2000 Key

leukocyte dyscrasia; thermal injury; cytokine-induced toxicity; ds. Crohn's disease; ulcerative colitis; necrotizing enterocolitis; inflammatory dermatosis; contact dermatitis; atopic dermatitis; psoriasis; urticaria; fever; myalgia; meningitis; encephalitis; Siggren's syndrome; alcoholic hepatitis; bacterial pneumonia; ypovolemic shock; Type 1 diabetes mellitus; hypersensitivity; chronic glomerulonephritis; inflammatory bowel disease;

Homo sapiens.

Location/Qualifiers 63..1814 Ø /*tag=

/product= "hPARP2"

16-JUN-2000; 2000WO-US16629

99US-0139543 16-JUN-1999;

(ICOS-) ICOS CORP.

Goldman PS, McElligott DL; Christenson E, Demaggio AJ,

WPI; 2001-025335/03. P-PSDB; AAB47029 New human poly(ADP-ribose) polymerase for treating inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte metastasis

Claim 1; Page 91-93; 129pp; English.

This sequence encodes human poly(ADP-ribose) polymerase (HPARP2).

This protein causes the covalent addition of polymers of ADP-ribose
to protein targets. HPARP2 activity is induced in many instances of
oxidative stress or during inflammation where there is direct damage
to the DNA. HPARP2 may be used to identify antagonists which
may be used to treat a human having a disorder mediated by PARP2
may be used to treat a human having a disorder mediated by PARP2
or neoplastic tissue growth disorders, e.g. ischemic stroke,
cor neoplastic tissue growth disorders, e.g. ischemic stroke,
transplantation, cerebral vasospasm; rheumatorid, osteo- or gouty
arthritis, spondylitis; Behcef's disease; sepsis, septic or endotoxic
shock, gram negative or positive sepsis, toxic shock syndrome; multiple
organ injury syndrome secondary to septicemia, trauma, or hemorrhage;
allergic or vernal conjunctivitis, uveitis, thyroid-associated
cophthalmopathy; eosinophilic granuloma; asthma, chronic bronchitis,
allergic rhintis, ARBS, chronic obstructive pulmonary disease,
silicosis, pulmonary sarcoidosis, pleuriss, alveolitis, reserving or
injury of the myocardium, brain or extremities; greated in the procession of formation ears tiseue formation experienced. fundation, scar tissue formation; attentions attentions as yestemic lupus erythematosus, autoimmune thyroiditis, multiple sclerosis; Reynaud's syndrome; graft versus host disease, allograft rejection; chronic glomerulonephritis; inflammatory bowel disease, Crohn's disease, ulcerative colitis, necrotizing enterocolitis; inflammatory dermatoses, antigen-antibody complex mediated diseases; hypovolemic shock; Type I diabetes mellitus; cute and delayed hypersensitivity; disease states due to leukocyte dyscrasia and metastasis; thermal injury; granulocyte transfusion associated syndromes; and cytckine-induced toxicity. hPARPP2 and antibodies to it, can also be used to diagnose these contact or atopic dermatitis, psoriasis, urticaria, fever and myalgias due to infection; meningitis, encephalitis, and brain and spinal cord Injury due to minor trauma; Sjogren's syndrome; diseases involving leukocyte diapedesis; alcoholic hepatitis; bacterial pneumonia;

Sequence 1814 BP; 558 A; 389 C; 462 G; 405 T; 0 other;

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                                                                                       1506 acaggactgctgctcttatcagaggtagctctaggtcagtgtaatgaactactagaggcc 1565
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                                                                                                                     999ctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
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                                 9; Gaps
                                                          1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60
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                                                                                                                                                                                                                                                                                                                                                                                                              352 ggcaagccggtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtc
    DB 22; Length 1814;
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Score 122.6; DB 22; Length
Pred. No. 9e-31;
); Mismatches 194; Indels
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 25.9%;
56.9%;
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                             Matches 268; Conservative
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                Similarity
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Fri Mar

WPI; 2000-087218/07 P-PSDB; AAY51174

Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease conditions -

Claim 7a; Page 49-52; 96pp; German.

This invention describes novel human and murine poly(ADP-ribose)
polymerase (PARP) homologues, which are characterised by an amino acid
solution with a functional NRD⁺-binding site and no zinc finger
sequence motif, of general formula CX_ZCX_ZMHX_ZC (I). The nucleic acid
sequences, PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
C PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which is the result of a PARP protein, especially an
energy deficiency, which may comprise tissue damage from cell death
founding necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative illness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence encodes the
human PARP2 protein used in the method of the invention.

Sequence 1843 BP; 599 A; 377 C; 447 G; 420 T; 0 other;

5 1587 agtgacacaggaattctgaatccagatggttataccctcaactacaatgaatattgta 1646 1467 aatootaaaggoogaaggattgottoaaggtaaacatagcaccaaggggotgggcaagatg 1526 1527 gotoccagttotgoccacttogtcaccctgaatgggagtacagtgccattaggaccagca 1586 1227 aacaggatgettetatggeatggtteeaggatgagtaactgggtgggaatettgageeat 1286 1347 tactitgetgacatgicticcaagagigccaattacigcitigccictcgcctaaagaat 1406 181 gtaggittgatgcitctitctgaggitgcittaggagacaigtatgaactaaagaaagcc 240 298 gigccaciggagicagagittg-----tgaagiggagggatgatgtcgtagitcccigc 351 352 ggcaagccggtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtc 411 121 tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct 180 241 acgiccaiggacaa---acciccaagaggaagcaiicgaccaagggailaggcaaaacc 297 25.9%; Score 122.6; DB 21; Length 1843; 56.9%; Pred. No. 9e-31; tive 0; Mismatches 194; Indels 9; Gaps 1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60 1647 tataaccccaaccaggtccgtatgcggtaccttttaaaggttcagtttaat 1697 412 tacaacacatcccaggtgaagatgcagttcttgctgaaggtgcgtttccat 462 Matches 268; Conservative Similarity Query Match Best Local q P δ 셤 ŏ q g õ qq οy ö ò à õ

Human brain poly-ADP-ribose-polymerase cDNA. AAC82090 standard; cDNA; 1843 BP 02-MAR-2001 (first entry) AAC82090; RESULT 15 AAC82090

cerebroprotective; antiparkinsonian; nephrotropic; cardiant; vasotropic; anticonvulsant; cytostatic; antibacterial; immunosuppressive; treatment; antinflammatory; antirheumatic; antiarthritic; antidiabetic; epilepsy; 2H-phthalazin-1-one derivative; neurodegenerative disease; tumor; neuronal damage; Alzheimer's disease; Huntington's disease; metastasis; parkinson's disease; ischemic damage; microinfarction; sepsis; Human; poly ADP-ribose polymerase; PARP; neuroprotective; nootropic; diabetes mellitus; ss.

Homo sapiens.

DE19921567-A1

16-NOV-2000.

99DE-1021567. 11-MAY-1999;

99DE-1021567

11-MAY-1999;

(BADI) BASF AG.

Lubisch W, Sadowski J, Kock M, Hoeger T;

WPI; 2001-032983/05. P-PSDB; AAB11480. Drugs for inhibiting PARP or especially homologous enzymes comprising 4-substituted phthalazinone derivatives, useful e.g. for treating neurodegenerative disease, ischemic damage, tumors or diabetes

Example A; Page 9-12; 14pp; German.

c derivatives (1) which are used for the treatment or prophylaxis of derivatives (1) which are used for the treatment or prophylaxis of diseases associated with elevated poly. (ADP-ribose)-Polymerase (PARP) (1) which are used for the invention have noctropic, also activity. The products of the invention have noctropic, activity, The products of the invention have noctropic, cardiant, vasotropic, anticonvulsant, cytostatic, antibacterial, immunosuppressive, antiflammatory, antirheumatic, antiatrhrittic, immunosuppressive, antiflammatory, antiphematic, antiatrhitic, immunosuppressive, respectially used for treating or preventing or preventing neurodegenerative disease or neuronal damage (specifically associated with ischemia, trauma or massive bleeding, especially appoplaxy or parkinson's disease, treating or preventing ischemic damage of specifically generalized epileptic attacks (e.g. petit mal and confidentially peneralized epileptic attacks (e.g. temporal lope populates) and attacks), treating microinfarction (e.g. during and after heart valve replacement, aneurysm resectioning and heart transplantation), revascularization of critically constricted coronary transplantation), revascularization of critically constricted coronary transplantation), revascularization of critically constricted coronary transplantations, after heart was expected myocardial ischemia and damage or after its mechanical or drug-induced lysis and treating tumors and confident park (i.e. the known form designated PARP), they especially inhibit park (i.e. the known form designated PARP), they especially the contribution of microinfactivity for PARP2 relative to microinfactor of more than 5). This invention describes novel 4-substituted 2H-phthalazin-1-one

Sequence 1843 BP; 599 A; 377 C; 447 G; 420 T; 0 other;

474

9; Gaps 25.9%; Score 122.6; DB 22; Length 1843; 56.9%; Pred. No. 9e-31; tive 0; Mismatches 194; Indels 9; Matches 268; Conservative Similarity Query Match Best Local S

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us-09-236-995d-3.rng

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1 gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcc		tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct		181 graggittgatgcttcttctgaggttgctttaggagacatgtatgaactaaagaaag		241 acgtccatggacaaacctccaagagggaagcattcgaccaagggattaggcaaaacc	1467 aatcctaaggccgaaggattgcttcaaggtaaacatagcaccaagggctgggcaagatg	298 gigccaciggagicagagitigigaagiggagggaigaigicgiagitcccigc		352 ggcaagccggtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtc		412 tacaacacatcccaggtgaagatgcagttcttgctgaaggtgcgtttccat 462	
61	1287	121	1347	181	1407	241	1467	298	1527	352	1587	412	1647
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Search completed: March 7, 2002, 18:16:38 Job time: 13288 sec

us-09-236-995d-3.rni

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

March 7, 2002, 16:49:07; Search time 122.78 Seconds (without alignments) 874.333 Million cell updates/sec Run on:

1 aacaagatgctattatggca......gtttccatcacaagaggtag 474 US-09-236-995D-3 Perfect score: Title:

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodate/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodate/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodate/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodate/2/ina/6B_COMB.seq:*
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SUMMARIES	ID	's edneuce 5,	7	-08-044-618-3 Sequence	-216 Sequence 216	Sequence	4 Sequence 14,	-26 Sequence 26,	-08-357-533A-1 Sequence 1,	Sequence 1,	Sequence I,	12,	-09-081-345-1 Sequence 1	so sequence 20,	us-08-457-176-1 Sequence 1, Appli	Sednence 1,	seguence 26,	26, 4	7 Sequence 227,	.328-111-685 Sequence 685	-219-7 Sequence 7,	.927-219-1 Sequence 1,	-927-219-3 Sequence 3,	US-08-927-219-5 Sequence 5, Appli	-219-126 Sequence 1	52465-10 Patent No. 52	Sequence	2 000000000
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Query Match

29.4%; Score 139.4; DB 1; Length 3747;
Best Local Similarity 57.6%; Pred. No. 2.6e-37;
Matches 270; Conservative 0; Mismatches 196; Indels 3; Gaps

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Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 32, Appli Sequence 22, Appl Sequence 22, Appl Sequence 58, Appl Sequence 58, Appl Sequence 65, Appl Sequence 65, Appl Sequence 67, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl		PREDISPOSITION TO RESTRICTION FRAMMENT LENGTH INE FOR THE HUMAN POLY (ADP-RIBOSE) FOX #1.25
US-08-651-472-2 US-08-551-472-3 US-08-358-928-2 US-08-358-928-3 US-07-750-080A-22 US-08-651-472-22 US-08-232-197-58 US-08-232-197-58 US-08-531-472-65 US-08-358-928-65 US-08-358-928-65 US-08-358-928-65 US-08-358-928-63 US-08-651-472-62 US-08-651-472-62 US-08-651-472-62 US-08-651-472-63 US-08-651-472-63 US-08-651-472-63 US-08-651-472-63 US-08-651-472-64 US-08-651-472-64	ALIGNMENTS	DETECTING A THE USED OF SM OF THE GE Goldstein & Ite 300 44,618 57,696 57,696
ろうよみこう みみみうりうけん サーラヤ		RRK RHOD OR RHOD OR REB BY LYWER BY LYWERAS LYMERAS SESIEr, ICUL Sul ALISK elease AR: OS/NB 6 6 70.353 30.353 30.353 1001 1001 1001 1001 1001 1101 1115
1133 11133 11133 11209 1209 3098 3098 3878 4145 4145 4277 4659 4701		lication US/0804 605 ATION: SMULSON, MARK ENTION: CANCER ENTION: POLYMOR ENTION: POLYMOR GUENCES: 7 (CE ADDRESS: 7 (CO NUMBER: US/06 (CON NUMBER: US/
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00000000000000000000000000000000000000		RESULT . 1  GO-08-044-618-5  Sequence 5, A  Patent NO. 54  GENERAL INFO  GENERAL INFO  APPLICAMTI  TITLE OF I  CORRESPOND  ADDRESSE  STATE:  COMPUTER  COMPUTER  COMPUTER  COMPUTER  COMPUTER  MEDIUM T  COMPUTER  COMPUTER  COMPUTER  COMPUTER  COMPUTER  COMPUTER  COMPUTER  COMPUTER  MEDIUM T  APPLICAM  FILING I  ATTORNEY APPLICAM  TELEPHOI
0 0 0 0 0 0 0		M D T T T T T T T T T T T T T T T T T T

STRANDEDNESS: both TOPOLOGY: linear MOLECULE TYPE: DNA US-08-044-618-7

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METHOD OR DETECTING A PREDISPOSITION TO CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)
                    2756 AACCGAAGATTGCTGTGGCACGGTCCAGGACCACCAACTTTGCTGGATCCTGTCCCCAG 2815
                                                                                         gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                                                                               121 tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct 180
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                                                                                                                                                                                                                                                                                                                                                                 301 ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcgggcaagccg 360
                                                                                                                                                                                                                                                                                          241 acgiccaiggacaaacciccaagagggaagcaticgaccaagggatiaggcaaaaccgig 300
1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60
                                                                                                                                                                                                                                                                                                                                                                                                                                       361 gigocaicaicaatiaggagototgaacicaigiacaaigagiacaicgictacaacaca 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3173 GCTCAGGTAAATCTGAAGTATCTGCTGAAACTGAAATTCAATTTTAAGA 3221
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STREET: 1225 Connecticut Suite 300
CITY: Washington
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APPLICATION NUMBER: US/08/044,618
FILING DATE: 19930406
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APPLICATION NUMBER: US/07/257,696
FILING DATE: 14-OCT-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 7, Application US/08044618

Patent No. 5449605

GENERAL INFORMATION:
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REGISTRATION NUMBER: 30,353
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SMULSON, MARK
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: POLYMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202)466-0800
TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 5345 base pairs
NUCLEIC ACID
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METHOD OR DETECTING A PREDISPOSITION TO CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE) POLYMERASE
                                                                                                                                             3519 AACTGAAGGTTGCTGTGGCATGGGTCCAGGACCACCAACTTTGCTGGGATCCTGTCCTG 3578
                                                                                                                                                                                                                                                       3639 TATITCGCTGATCTTGTCTCCAAGAGTGCCAACGACTGCCATACATCTTAGGAAGACCCA 3698
                                                                                                                                                                                                                                                                                                                 3759 TCACATATCAGCAAGTTACCCAAGGGCAAGCACAGTGTCAAAGGTTTGGGCAAAACTACT 3818
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                                                                     1 aacaagatgctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaa 60
   DB 1; Length 5345;
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                                        Indels
                 Pred. No. 1.1e-36;
0; Mismatches 197;
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 Score 137.8;
Pred. No. 1.1
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FILING DATE: 14-OCT-1988
ATTORNEY/AGENT INFORMATION:
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19930406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/08044618
; Patent No. 5449605
Query Match
Best Local Similarity 57.48;
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CORRESPONDENCE ADDRESS:
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                                Matches 269; Conservative
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1225 ConneCITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                         Score 136.2; DB 1; Length 2682;
Pred. No. 2.7e-36;
0; Mismatches 198; Indels 3;
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APPLICANT: Lewis, Marcia E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILLE REFERENCE: CCD-257 (US)
                                     0654.0490001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 216, Application US/09328111 Patent No. 6262333 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Endege, Wilson O. APPLICANT: Endege, Wilson O. APPLICANT: Astle, Jon H. APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E. APPLICANT: Carroll III, Eddie APPLICANT: Carroll III, Eddie APPLICANT: Catino, Theodore J.
NAME: FOX, SAMUEL L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0654.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)466-0800
TELEFAX: (202)483-8716
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2682 base pairs
                                                                                                                                                                                                                                                                                             query Match 28.7%;
Best Local Similarity 57.1%;
Matches 268; Conservative (
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                                                                                                                                                                    TYPE: NUCLEIC ACID STRANDEDNESS: both
                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                           MOLECULE TYPE: DNA
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METHOD OR DETECTING A PREDISPOSITION TO CANGER BY THE USED OF RESTRICTION FRAMMENT LENGTH POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE) POLYMERASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 graggittgaigcitcittctgaggitgcittaggagacaigtaigaactaaagaaagcc 240
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                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                       DB 4; Length 595;
                                                                                                                                                                                                                                                                                                       24.2%; Score 114.6; DB 4; Length 963.3%; Pred. No. 2.6e-29; tive 0; Mismatches 109; Indels
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CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIEN FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 216
LENGTH: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1225 Connecticut Suite 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,618
FILING DATE: 19930406
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; Patent No. 5449605
                                                                                                                                                                                                                 ; LOCATION: (1)...(595); OTHER INFORMATION: n = A,T,C or G US-09-328-111-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SMULSON, MARK
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: POLYMO
TITLE OF INVENTION: POLYMO
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                 Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SMULSO
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STATE: D.C.
20036
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                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1389 ATAGGGTTAATCCTGTCGGAAGAAGTTGCCCTTGGAAACGTGTGTGAACTGAAGCATGCT 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 aacaagatgctattatggcacggttcaaggttgacgaattttgtggggaattcttagtcaa 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 acgtccatggacaaacctccaagagggaagcattcgaccaagggattaggcaaaac 296
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Score 108.8; DB 1;
Pred. No. 3.9e-27;
0; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FEAKINER, F. G.
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1800 Diagonal Road, Suite 500
  APPLICATION NUMBER: US/07/257,696
FILING DATE: 14-OCT-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/232,463
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Patent No. 5670367
                                                                            REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 065
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                 TELEPHONE: (202)466-0800
TELEFAX: (202)33-8716
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    LENGTH: 1592 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USE Z13-029
ZIP: Z2313-0299
COMPUTER READABLE FORM:
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                                                                SAMUEL L
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-044-618-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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88 cctgttactggctatatgttcggcaaaggcctctactttgcagatctagtaagcaagagc 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.5%; Score 31; DB 1; Length 7218
Best Local Similarity 6.1%; Pred. No. 2;
Matches 25; Conservative 198; Mismatches 188; Indels
                                                                                        REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calfee, Halter & Griwold LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kniss, Douglas A.
TITLE OF INVENTION: Elcosanoid Formation
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/08627254C Patent No. 5859229 GENERAL INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         29,768
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                                                                                                                                          TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
               FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                               (703)836-9300
                                                                                                                                                                                                                     7218 base pairs
                                                    NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                      US-08-232-463-14
                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                         TOPOLOGY: line IMMEDIATE SOURCE:
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                                                                                                                               TELEPHONE:
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us-09-236-995d-3.rni

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Sequence 1. Application US/08459009
Sequence 1. Application US/08459009
Sequence 1. Application US/08459009
Sequence 1. Sedilary
APPLICANT: JIN, DONALD F
APPLICANT: SMARY JOHN E
APPLICANT: SWARY JOHN E
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
NUMBER OF SEGUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
ADDRESSEE: INC
                                                                                                                                                                                                                                                                                                            Query Match 6.4%; Score 30.4; DB 2; Length 2625; Best Local Similarity 55.8%; Pred. No. 1.9; Matches 58; Conservative 0; Mismatches 46; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /product= "DROSOPHILA MORPHOGEN CHER INFORMATION: RECEPTOR" US-08-357-533A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/357,533
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: CRP-073FW
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (508)-435-9001
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MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2625 base pairs
                     LENGTH: 2625 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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SEOUENCE CHARACTERISTICS:
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EDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                  NAME/KEY: CDS
FOCATION: 379..1929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01748
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6.5%: Score 30.6; DB 2; Length 2757;
Best Local Similarity 56.4%; Pred. No. 1.7;
Matches 57; Conservative 0; Mismatches 44; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: JIN, DONALD F
APPLICANT: OPPERANN, HERMANN
APPLICANT: OPPERANN, HERMANN
APPLICANT: SMART, JOHN E
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: GOLICK, MAY E
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 18525/00107
TELECOMMUNICATION INFORMATION:
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERIFICS:
LENGTH: 2757 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/357,533A FILING DATE: 16-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRP-073FW
                                               APPLICATION NUMBER: US/08/627,254C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-08-357-533A-1/C
'Sequence 1, Application US/08357533A
'Patent No. 5831050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)-435-9001
TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,637
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 45 SOUTH STREET CITY: HOPKINTON STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ANTI-SENSE:
US-08-627-254C-26
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                                                                                                                                                                      Gaps
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0
                                                                                                                          6.4%; Score 30.4; DB 2; Length 2625; 55.8%; Pred. No. 1.9; tive 0; Mismatches 46; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/0845951
Patent No. 609347
GENERAL INFORMATION:
APPLICANT: JUN DONALD F
APPLICANT: OPPERMANN, HERMANN
APPLICANT: SMART, JOHN E
TITLE OF INVENTION: NOVEL MORPHOGEN CELL SURFACE RECEPTOR NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES,
                                                                                                                                                                                                                                                                         ; LOCATION: 379..1929
; OTHER INFORMATION: /product- "DROSOPHILA MORPHOGEN
; OTHER INFORMATION: RECEPTOR"
US-08-459-009-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "DROSOPHILA MORPHOGEN RECEPTOR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/357,533
FILING DATE: 16-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: KELLY, ROBIN D
REGISTRATION NUMBER: 34,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/459,951
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (508)-435-0992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (508)-435-9001
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STREET: 45 SOUTH STREET
CITY: HOPKINTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2625 base pairs
                                                                                                                                               Best Local Similarity 55.8
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379..1929
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COTHER INFORMATION:
US-08-459-951-1
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NAME/KEY:
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                                                                                                                             Query Match
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                                                                                     125 ttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcctgtag 184
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                                                 0; Gaps
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0
      Score 30.4; DB 3; Length 2625;
Pred. No. 1.9;
0; Mismatches 46; Indels 0
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Pred. No. 2;
0; Mismatches 22; Indels 0;
                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SELICATION NUMBER: US/07/780,973
FILING DATE: 19911023
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: PEAKMAN DR., TIMOTHY C
APPLICANT: PAGE DR., MARTIN J
APPLICANT: CHARLES DR., IAN G
TITLE OF INVENTION: EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: 14TH FLOOR
STREET: 2200 CLARENDON BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 9023111.9
                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/07780973 Patent No. 5322774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CRAWFORD MR., ARTHUR R
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 510-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703) 8750400
TELEFRX: (703) 5253468
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 15:
          6.4%;
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Best Local Similarity 66.2%;
Matches 43; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1160 base pairs
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19911023
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID STRANDEDNESS: both
Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON STATE: VIRGINIA
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945 TGATG 949
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                                                                                                                                                                                                                                                                   RESULT 11
US-07-780-973-15
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US-07-780-973-15
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EARLIER APPLICATION NUMBER: US 08/433,111
                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0 - beta
                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197430 BBMB UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                 SEQ ID NO 20
LENGTH: 1743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX:
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                                                                                                                                                                                                                                                                                                      FEATURE
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APPLICANT: Fischhoff, David A.
TITLE OF INVENTION: Synthetic Plant Genes and Method for Preparation
FILE REFERENCE: 38-21(15119)A
CURRENT APPLICATION NUMBER: US/08/841,178
CURRENT FILING DATE: 1997-04-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.2%; Score 29.4; DB 4; Length 3580; Best Local Similarity 56.8%; Pred. No. 5;
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                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Bahija Jallal
APPLICANT: Bragory D. Plowman
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: PTP04 RELATED DISORDERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 ggtgaagatgcagttcttgctgaaggtgcgtttcc 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: MAY 20, 1997
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FASLSEQ for Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/081,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08841178 Patent No. 5880275
                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                             Sequence 1, Application US/09081345 Patent No. 6228641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3580 base pairs
TYPE: nucleic acid
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CITY: Los Angeles
STATE: California
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US-09-081-345-1
                                                                                                                                                                                                                                                                                                                                                                                                    X: U.S.A.
90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                US-09-081-345-1
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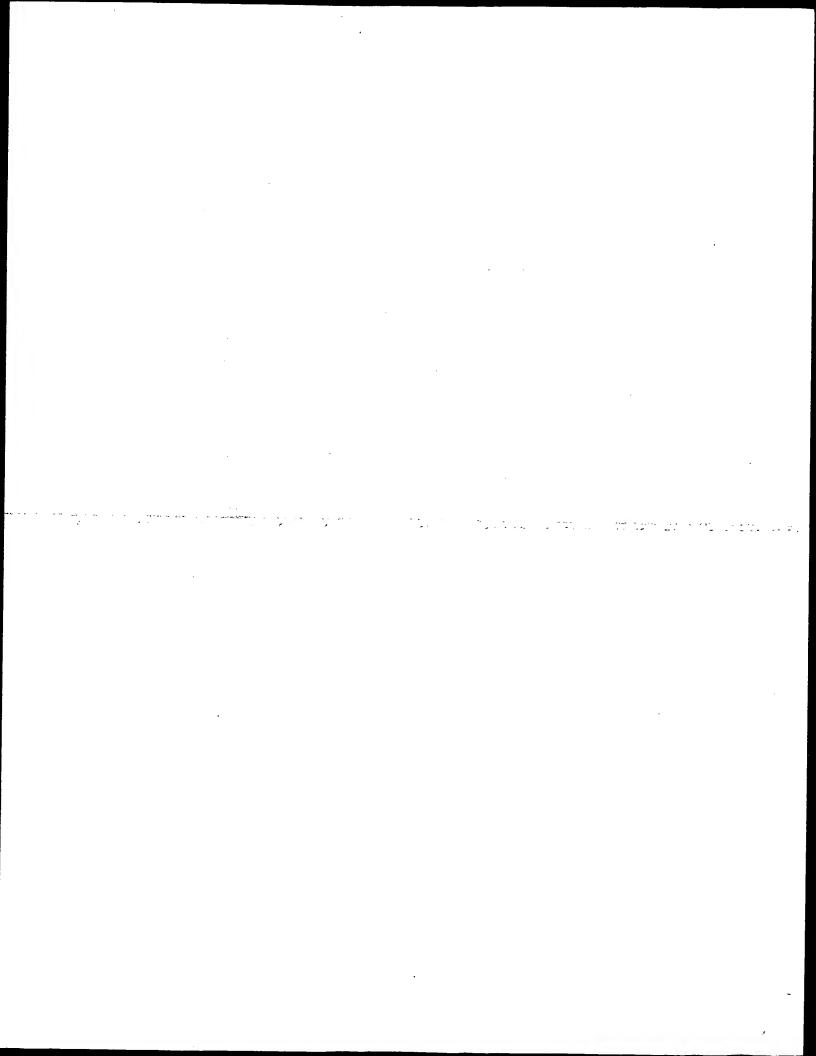
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1345 GGATITGGGTGATTTGTGATGAAGGGATGATGTTGTTGAACTCAGCACTACGATGTATCC 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 ggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccggtgcc 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: structural gene encoding B.t.k. HD-1 insectidal OTHER INFORMATION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 56.4%; Pred. No. 7.5;
Matches 53; Conservative 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
APPLICANT: de la Chappelle, Albert
TITLE OF INVENTION: Mutator Gene and Hereditary
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Banner, Birch, McKie, and Beckett
STREET: 1001 G Street, N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 atcatcaattaggagctctgaactcatgtacaat 399
EARLIER FILING DATE: 1995-05-03
EARLIER FILING DATE: 1995-06-03
EARLIER FILING DATE: 1992-10-09
EARLIER FILING DATE: 1992-10-09
EARLIER FILING DATE: 1990-02-12
EARLIER FILING DATE: 1990-02-12
EARLIER FILING DATE: 1990-02-12
EARLIER FILING DATE: 1989-02-24
NUMBER OF SEQ ID NOS: 27
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.44900
TELECOMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELEPHONE: 202.508.9299
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01-UUN-1995
0N: 530
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APPLICATION NUMBER: US 08/160295
FILLING DATE: 02-DEC-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5591826
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) ORIGINAL SOURCE: ORGANISM: Homo sapiens US-08-457-175-1

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Patent No. 5693470

GENERAL INFORMATION:
APPLICANT: Wogelstein, Bert
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Minzler, Kenneth W.
APPLICANT: Minzler, Kenneth W.
TILLE OF INVENTION: Mutator Gene and Hereditary
TITLE OF INVENTION: No. 5693470-Polyposis Colorectal Cancer
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie, and Beckett
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                   6.0%; Score 28.4; DB 1; Length 2947; 60.3%; Pred. No. 9.8; tive 0; Mismatches 31; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.44900
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9100
TELERX: 202.508.9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/457,175
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160295
FILING DATE: 02-DEC-1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
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                 LENGTH: 2947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 60.3%
Matches 47; Conservative
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LENGTH: 2947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  ; ORGANISM: Homo sapiens US-08-457-176-1
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                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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USA
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ORIGINAL SOURCE:
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BF255013 HVSMEf000
BE419432 WWS012.A1
AV834168 AV834168
BE420229 WWS04.C11
BG042229 SU93C12.Y
BE941860 EST421439
AV833893 AV833893
D42790 D42790 Rice
BI217470 602933675
BE911127 601662539
BIO779902 602876096
BE304535 601105502
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1735.730 Million cell updates/sec
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                                                             March 7, 2002, 15:24:26; Search time 2934.5 Seconds
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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BE420229
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Maximum DB seq length: 200000000
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269.2
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AA401836 zt86c12.r BA401836 zv66b12.r BB703436 602859629 BF703750 601255121 BER10170 601753112 BER2179 601297572 BG675913 601297572 BA675913 601297572 AA463755 LD07027.5 AA463755 LD07027.5 AA463755 LD07027.5 AA463755 LD07027.5 BG78918 LD07037.3 BG78910 602401166 BF7042005 BP250013A BG701594 60150130 BG701594 60150130 BG701594 602299739 BG701594 60225914 BG429402 602499622 BE123437 946002D04 BB123437 946002D04 BG79139 946002D04 BG79155 602139160 BG751755 602130481 BI199670 602763286 BE199670 602763286 BE198132 177421 BA AA417842 tg72a07.x AA212857 mw84d01.r BG303304 f151b10.x AA608364 vm89h12.r AA608364 vm89h12.r AA608364 vm89h12.r
AA397988 AA401836 BE703705 BE703705 BE701770 BE382739 BE782739 AA14795 AA267755 AA267755 AA267755 AA267755 AA26775 BE7020745 BE7020745 BE703020 BE703020 BE703020 BE703020 BE102437 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470 BE102470
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78 4 5 7 8 6 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7
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## ALIGNMENTS

RESULT 1 BF255013	
LOCUS	BF255013 607 bp mRNA EST 23-FEB-2001 HVSMFf0005L18f Hordeum vulgare seedling root EST library HVcDNA0007 etiolated and unstressed) Hordeum vulgare cDNA clone HVSMFf005f1.8f. mRNA sequence.
ACCESSION VERSION KEYWORDS	BF255013.2 GI:13117445 EST.
SOURCE	barley. Hordeum vulgare Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae : Triticeae: Hordeum.
REFERENCE AUTHORS	1 (bases 1 to 607) Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu , Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo , T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
TITLE	Development of a genetically and physically anchored EST resource for barley genomics
JOURNAL COMMENT	Unpublished (2000) On Nov 16, 2000 this sequence version replaced gi:11184130. Contact: Wing RA Clemson University Genomics Institute
	Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Small: raing@clemson.edu Gen primer: AgarpaAgaCramsanAgaCramsan.edu
FEATURES SOUTCE	High quality sequence stop: 551.  Location/Qualifiers 1607 /organism="Hordeum vulgare"

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Zeneca Wheat Improvement Centre, Norwich Research Park Colney Lane, Norwich NR4 7UH UNITED KINGDOM Tel: 44 1603 250 2600
Fax: 44 1603 699
Email: wolfgang.schuch@aguk.zeneca.com
International Triticeae EST Cooperative (ITEC)
Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 CAGGTGAAGATGCAGTTCTTGTTGAAGGTCAGATTCCGTCACAAGCGTT 413
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                                                                                                                                                                                                                                                                                                  http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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                              Unpublished (2000)
Contact: Schuch W
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1 (bases 1 to
Sato, K.
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1 (bases 1 to 536)
Anderson,O.A., Appels.R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Galle,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Warburton,M. and Wenzel,G. Shariflou,M., Solvells,M., Marburton,M. and Wenzel,G. Production of
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see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 actggctatatgttcggcaaaggcctctactttgcagatctagtaagcaagagcgcacaa 153
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Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann, R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Lonpublished (2000)
Contact: Schuch W. Zeneca Wheat Improvement Centre, Norwich Research Park Colney Lane, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 250 2600
Fax: 44 1603 250 2600
Fax: 44 1603 250 2600
Fax: 44 1603 250 Choperative (ITEC)
International Triticeae EST Cooperative (ITEC)
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8933612, Y1 Gm-G1055 Glycine max cDNA clone GRNOME SYSTEMS CLONE ID:
Gm-C1055-2064 5' similar to TR:Q92P54 Q92P54 POLY(ADP-RIBOSE)
POLYMERASE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="scutellum callus"
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/db_xref="taxon:4565"
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Spernatophyta: Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 369)
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                                                                                                                                                                                                                                                                                                                        /clone="rbags5k04"
/clone=lbb="k. Sato unpublished cDNA library: Hordeum
vulgare subsp. vulgare shoots germination"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agaattgcacctcctgaggcacctgtta-ctggctatatgttcggcaaaggcctctactt 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                  Unpublished (2001)
Contact: Razuhiro Sato
Contact: Razuhiro Sato
Contact: Razuhiro Sato
Cokayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiti, Okayama 710-0046, Japan
Bmail: kazasatoërib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 catggacaaacctccaagagggaagcattcgaccaagggattaggcaaaaccgtgccact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                         database:http://www.shigen.nig.ac.jp/barley/Barley.html.
    Barley EST sequencing project in NIG and Okayama Univ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 661;
                                                                                                                                                                                                                                                             /organism="Hordeum vulgare subsp. vulgare"
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/db_xref="taxon:112509"
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Pred. No. 1.1e-79;
0; Mismatches 60;
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181 c 132 g 168
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85.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anote—"Oscillation of the planescript II SK+; Site_I: EcoRI; Site_2: Ahote—"Oscillation mature seed pods of greenhouse grown plants prior to senescence for the cultivar KPI. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(df) sequence with a XNoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directioned into the EcoNI. About restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
linsert Length: 429 Std Error: 0.00
High quality sequence stop: 419.
                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Mature seed pods, greenhouse grown"
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                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Cote, F., Ojanen-Reuths, T., Hahn, M.G., VandenBosch, K., Hur, J.,
Børemand, P., Endre, G., Town, C.D., Bøwman, C.L., Craven, M.B. and Cho
J., From seedling roots of Medicago truncatula after treatment
with beta glucan elicitor preparation from Phytophthora sojae
Unpublished (2000)
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hahn@ccrc.uga.edu
University of Georgia name: G269712e TIGR sequence name: MTJAP09TK
More information is available at: http://chrysie.tamu.edu/medicago
Seq primer: Sknod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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EST421439 MGHG Medicago truncatula cDNA clone pMGHG-6B18, mRNA
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242 GTTCTGAGCTCATGACAATGAGTATATTGTTTATAATACTGCTCAAGTTAAGATGCAAT 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Indels
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220 Riverbend Road, Athens, GA 30602-4712, USA
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74.9%; Pred. No. 1.2e-45;
Live 0; Mismatches 78
                                                                                                                                                      440 tettgetgaaggtgegttteeatcacaagaggt 472
                                                                                                                                                                                                              302 TCTTATTGAAGGTGAGGTTTCATCACAAGAGAT 334
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/db_xref="taxon:3880"
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Matches 233; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D42790 442 bp mRNA EST 04-MAY-1998
D42790 Rice callus cDNA (H.Uchimiya) Oryza sativa cDNA clone 285,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 gaataateetgtaggtttgatg--ettetttetgaggttgetttaggagacatgtatgaa 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 ct---aaagaaagccacgtccatggacaaa-cctccaagagggaagcattcgaccaaggg 284
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513 TACTTTGCCGATATGTTCTCCAAGAGTGCAAACTACTGCTATGCTTCACAAACATCTAGA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAAAACCCAGTNGNTTTNATGCCCTCTTCCCCAAGGTTGCCCCCAGTNACATGTATGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute of Mol. & Cell. Bioscience, Department of Cellular Function
                                       241 acgtccatgg---acaaacctccaagaggaagcattcgaccaagggattaggcaaaacc
                                                                                                                                                          393 AAGTACGATGCTAATAACCTGCCCAAGGGAAAACTAAGTACTAAGGGAGTTGGCCAGATG
                                                                                                                                                                                                 298 gtgccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcgggcaag
                                                                                                                                                                                                                     358 ccggtgccatcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaac
                                                                                                                                                                                                                                                                                                                  279 CCCAAAGAAGAACCTTCAAAGAGGGGTAGCTTGCTGTACAACGAGTACATTGTTTACAAC
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                                                                                                                                                                                                                                                                                                                                                                                219 GTAGAGCAGATCAGGATGCGGTACGTGCTCATGTTTCTTAACTTCAAGGG 167
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Tel: 03-3812-2111(ex.7844)
Fax: 03-3812-2910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%; Score 155.8; DB 1
76.8%; Pred. No. 1.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: huchimiy@tansei.cc.u-tokyo.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On nucleotide sequence of Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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/db_xref="taxon:4530"
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89 c 110 g
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Contact: Hirofumi Uchimiya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="285"
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Uchimiya, H.
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Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                          AV833893 661 bp mRNA EST 22-JUN-2001
AV833893 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
concerpaga10f19, mRNA sequence.
                                                                                                  240
                                                                                                                                       348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="rbags10f19"
/clone=lbb="k. Sato unpublished cDNA library: Hordeum
/clone_lbb="k. Sato unpublished cDNA library: Hordeum
/tissue_type="shoots"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Bmail: kazasatofrib.okayama-u.ac.jp, UBr.http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
                    tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct
                                                                                              289 GCTGGTCTAATGCTTTTGAGTGAAGTTGCCCTTGGAAATGTGTATGAGCTCAAAAAGCT
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    Location/Qualifiers
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Pred. No. 4.6e-38;
0; Mismatches 171; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
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179 c 133 g 164
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/db_xref="taxon:112509"
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Best Local Similarity 61.9%;
Matches 293; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       BI217470 716 bp mRNA EST 11-JUL-2001 602933675F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5096850 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 71a).

NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B (II phage=resistant)"
/lab_host="DH10B (II phage=resistant)"
/note="Organ: liver: Vector: pCWV-SPORT6; Site_l: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
121 NCTTAGGCAAAAACCCGTGCGCGCTCGAGTCTGAGTTTGCGAAATGGAGGGATGATGTTGT 180
                                                                                                                                                                   tactttgcagatctagtaagcaagagcgcacaatactgttatgtgggataggaataatcct 180
                                                                                                   181 GGTGCCATGCGGAAAGCCAGTGCCAGCATCTATCAAGACATCTGAGCTTATGTACAATGA 240
                                                                                                                                         402 gtacatcgtctacaaccacatcccaggtgaagatgcagttcttgctgaaggtgcgtttcca 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    342 agttccctgcggcaagccggtgccatcatcaattaggagctctgaactcatgtacaatga 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 AACCGGAGGCTGCTGTGGCACGGCTCCAGGACCACCAACTTTGCTGGCATCCTGTCGCAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 152.2; DB 11; Length
Pred. No. 2.8e-35;
0; Mismatches 188; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov
Plate: LLAM11232 row: f column: 19
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Location/Qualifiers
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Best Local Similarity 59.3%;
Matches 278; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                           462 tcacaagaggt 472
                                                                                                                                                                                                                                                                  301 TCACAAGAGGT 311
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ORIGIN
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KEYWORDS
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BE911127 587 bp mRNA EST 29-SEP-2000 601662539F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3962696 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases 1 to 5877)
NIH-WGC http://mgc.ncl.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                          360
                                                                                                                                                                                                                                                                                                                                                                   132 TACTITGCCGACATGGTGTCCAAAAGTGCAAACTACTGCCACACATCTCAGGGAGACCCG 191
                                             241 acgtecatggacaaacetecaagagggaagcattegaecaagggattaggeaaaaeegtg 300
                                                                                                                                                                                                                                                                                                                                       361 gigocaicaicaattaggagototgaacicaigiacaatgagiacaiogiotacaacaca 420
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                                                                                                                                                                                                                                            301 ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                       421 teccaggtgaagatgeagttettgetgaaggtgegttteeateacaaga 469
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Plate: LLAM9129 row: n column: 09
High quality sequence stop: 559.
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/tissue_type="tumor, blopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3962696"
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BE911127
BE911127.1 GI:10408111
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Best Local Similarity 59.1
Matches 277; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                121 tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imaga.llnl.gov.co.column: 24
                                                        61 gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
                                                                                          85 GGTCTGCGGATAGCCCCACCTGAAGCGCCTGTGACAGGCTACATGTTTGGGAAAGGGATC 144
                                                                                                                                                                      145 TACTTTGCCGACATGGTGTCCAAAAGTGCAAACTACTGCCACACATCTCAGGGAGACCCG 204
                                                                                                                                                                                                            241 acgtccatggacaaacctccaagagggaagcattcgaccaagggattaggcaaaaccgtg 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 725)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
20-JUN-2001
                                                                                                                                                                                                                                                                                                              265 TCACATATCAGCAAGTTACCCAAGGCAAGCACAGTGTCAAAGGTTTGGGAAAAAACC---
                                                                                                                                                                                                                                    205 ATTGCCTTAATACTGCTGGGAGAGGTTGCCCTTGGAACATGTATGAACTCAAGCATGCT
                                                                                                                                                                                                                                                                                                                                                              301 ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 tcccaggtgaagatgcagttcttgctgaaggtgcgtttccatcacaaga 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Mam2"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="PH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:5007983"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Marional Libration (1)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE304535 571 bp mRNA EST 13-JOUL-2000 601105502F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988216 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The 1.M.A.G.E. Consortium (LLNL) DNA Sequencing by: The 1.M.A.G.E. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov High quality sequence stop: 567.
                                                                                                                                                                                                                                                                                                                                                          129 agatotagtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggttt 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 gatgottotttotgaggttgctttaggagacatgtatgaactaaagaaagccacgtccat 248
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                                                                                                                                                                                                                                                                                                                                                                                       9 gctattatggcacggttcaaggttgacgaattttgtgggaattcttagtcaagggctaag
                                                                                                                                                                                                      2 GCTGCTGTGGCACGCTCCAGGACCACCAACTTTGCTGGCATCCTGTCGCAGGGTCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 CAGCAAGTTACCCAAGGGCAAGCACAGTGTCAAAGGTTTGGGAAAAACC---ACCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 gicagagitigigaagiggagggatgaigtegiagiteeeigeggeaageeggigeeate
                                                                                       Length 725;
                                                                                                                                 0; Mismatches 184; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 gaagatgcagttcttgctgaaggtgcgtttccatcacaaga 469
                                                                                       DB 11;
                                                                                    Score 150.6; DB 1 Pred. No. 8.7e-35;
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_15"
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                                                                                    31.8%;
59.4%;
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                                                                                                                               Matches 274; Conservative
  204
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TITLE
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Matches 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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/lab_host="DH10B (phage-resistant)"
/nate="Organ: colon, Vector: poTB7; site_1: XhoI; Site_2:
/note="Organ: colon, Vector: poTB7; site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dr priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size=selected 500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
47 a 140 c 140 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Contact: Wilson RK
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5' similar to gb:J03473 NAD(+) ADP-RIBOSXLTRANSFERASE (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 acgiccaiggacaaacciccaagagggaagcaiicgaccaagggaitaggcaaaaccgig 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 ATAGGCTTAATCCTGTTGGGAGAAGTTGCCCTTGGAAACATGTATGAACTGAAGCACGCT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 TCACATATCAGCAAGTTACCCAAGGCAAGCACAGTGTCAAAGGTTTGGGCAAAACTACC 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gggctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tactttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcct 180
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Pred. No. 2.1e-32;
0; Mismatches 194; Indels
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58.0%;
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AA397988
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Washington University School of Medicine

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LOCUS AA401836 669 bp mRNA EST 16-MAY-1997
DEFINITION 2v66b12.r1 Soares_total_fetus_ND2HF8_9W Homo sapiens CDNA clone
                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1320 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343 CCTGATCCTTCAG---CTAACATTAGTCTGGATGGTGTAGACGTTCCTCTTGGGACCGGG 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 IATTICGCIGACAIGGICICCAAGAGIGCCAACIACIGCCAIACGICTCAGGGAGACCCA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 AACCGAAGATIGCIGIGGCACGGICCAGGACCACCAACTIIGCIGGGAICCIGICCCAG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 2.1e-32;
0; Mismatches 194; Indels
                                                                                                                                             Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 427.
                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:592767"
/db_xref="taxon:9606"
/clone="IMAGE:729238"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                             Location/Qualifiers
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.1%;
                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
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1 (bases 1 to 669)
Hilliaria, Allen, Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, No., Lennon, G., Marra, M., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle
,T., Waterston, R. and Wilson, R.
Umpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pT713D-Pac (Pharmacia) with a modified Polylinker; Site_1: Not I; Site_2: Eco RI: 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - 011go(dT) priner [5' TGTIRCCAATCIGAAGTGGGAGGGCGCGTTAATTITTITTITTITTITT 3'].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
IMAGE:758591 5' similar to gb:J03473 NAD(+) ADP-RIBOSYLTRANSFERASE
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 Er from Amersham
High quality sequence stop: 493.
Location/Qualifiers
1. 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 142.6; DB 10; Length 669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_total_fetus_Nb2HF8_9w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:758591"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="8-9 weeks"
/lab_host="DH108"
                        (HUMAN);, mRNA sequence
                                                                       AA401836.1 GI:2055855
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58.0%;
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314 286 1810
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
                                                                                                                                                                                                                                                                                               BIO93436 916 bp mRNA EST 20-JUN-2001 602859629F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:5000911 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs.remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stop: 837.
Location/Qualifiers
361 gigccatcatcaattaggagcictgaactcatgtacaatgagtacatcgtctacaacaca 420
                                                                                                    557 ATTICATCTGGTGTGAATGACACCTCTCTACTATATAACGAGTACATTGTCTATGATATT 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 AACCGAAGATTGCTGTGGCACGGGTCCAGGACCACCAACTTTGCTGGGATCCTGTCCCAG 244
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Pred. No. 2.5e-32;
0; Mismatches 194; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_MGC_10"
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/clone="IMAGE:5000911"
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us-09-236-995d-3.rst

«	365 ATAGGCTTAATCCTGTTGGGAGAAGTTGCCCTTGGAAACATGTATGAACTGAAGCACGCT	424
241	acgtccatggacaaacctccaagaggaagcattcgaccaagggattaggcaaaaccgtg	00
	425 TCACATATCAGCAAGTTACCCAAGGGCAAGCGCACGTGTCAAAGGTTTGGGCAAAACTACC 484	84
	301 ccactggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccg	360
	485 CCTGATCCTTCAGCTAACATTAGTCTGGATGGTGTAGACGTTCCTCTTGGGACGGG	541
	361 gigocatcatcaattaggagcictgaactcatgtacaatgagtacatcgictacaacaca	420
	542 ATTCTGGTGTGAATGACACCTCTCTACTATAACGAGTACATTGTCTATGATT	601
	421 teccaggigaagaigeagitetigeigaaggigegiteeateacaaga 469	
	602 GCTCAGGTAAATCTGAAGTATCTGCTGAAATTCAATTTTAAGA 650	

Search completed: March 7, 2002, 15:24:30 Job time: 3340 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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using sw model nucleic search, nucleic

March 7, 2002, 14:32:50; Search time 4873.04 Seconds (without alignments) 9983.538 Million cell updates/sec Run on:

US-09-236-995D-1 2949 Perfect score:

1 atggcggcgccgccaaaggc.....gtttccatcacaagaggtag 2949 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1472140 seqs, 8248589755 residues Searched: 2944280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database

gb_htg:*
gb_in:*
gb_on:*
gb_ox:*
gb_ph:*
gb_ph:*
gb_ph:*
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gb_r:* em_fun:* em_hum:* gb_vi:* em_ba:* *:un-qb gb_sy:* gb_ba:*

em_pat:* em_sts:* em_ov:* em_ph:* em_om:* em_pl:* em_ro:* em_sy:* em_or:* 114. 115.:. 117.:. 119.:. 221.:. 224.:. 226.:. 229.:. 330.:.

em_in:*

em_htgo_hum:*
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em_htg_rod: * em_un: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. em_htg_other:*

X52690 Chicken mRN D90073 Bovine poly D14667 Frog mRNA f 212139 X.laevis PA M18112 Human poly( A52134 Sequence 1 J03473 Human place AF8878 Cricetulu X65497 R.norvegicu AX058340 Sequence AX052277 Sequence AX052277 Sequence 5 U14359 Sequence 5 U143 AC006593 Arabidops AX058336 Sequence AX058382 Sequence AX058380 Sequence L24094 Gorilla gor AJ336876 Homo sapi AF085734 Homo sapi AP003889 Oryza sat AK001980 Homo sapi AF051548 Drosophil AJ007780 Mus muscu AF072521 Mus muscu BC012041 Mus muscu AF126717 Mus muscu X14206 Mouse mRNA AC014613 Drosophil AE002892 Drosophil AX058338 Sequence AJ222588 Zea mays AJ236912 Homo sapi AX058317 Sequence AJ131705 Arabidops AX058362 Sequence Z48243 A.thaliana D16482 Sarcophaga AX008892 Sequence AX058374 Sequence D13806 Fruit fly 1 AF093627 Zea mays AJ222589 Zea mays ZMPARP2 ATH131705 GGPADPRP BOVPAS XELPADPRP HUMADPPO AF168781 BC012041 AF126717 SPEPADPRP HSA236912 DROADPRPA AK001980 DMPARP5 AE002892 AX058338 HUMRISDAD AX058340 AX062277 RNU94340 HSA236876 MMADPRP AX058362 AX058380 AX008892 AF085734 AX058317 AF093627 AX058374 HUMPOLP HUMPPOL XLPARPG ZMPARP1 ATPARP 10 1000 6 10 10 DB 3463 2295 1754 1814 1814 1874 3080 1910 1910 1980 1980 1980 1982 10988 10988 3640 3792 3795 1771 1939 3045 3660 3128 3845 1732 3172 3200 Query Match Length 79663 1707 0000000000004 2005.2 2004.4 2004.2 2000.2 191.8 191.8 191.8 191.6 190.2 1186.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 1183.2 239.2 238.2 224.6 224.6 224.6 223.3 2222.2 219.8 219.8 219.8 219.8 219.8 2117.4 216 212.4 . No Result

## ALIGNMENTS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 3285)
Mahajan, P.B. and Zuo, Z.
Mahajan, P.B. and cDNA cloning of maize Poly(ADP)-ribose polymerase Plant Physiol. 118 (3), 895-905 (1998) AF093627 3285 bp mRNA PLN 29-NOV-1998 Zea mays poly(ADP)-ribose polymerase (PARP1) mRNA, complete cds. AF033627 AF093627.1 GI:3928870 Zea mays. Zea mays KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL MEDLINE REFERENCE DEFINITION ACCESSION VERSION REFERENCE RESULT AF093627 LOCUS

2 (bases 1 to 3285) Mahajan, P.B. and Zuo, Z. Direct Submission AUTHORS TITLE

SUMMARIES

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KCTIELAPSARTSCRKOSEKITKGSVELSKEREEREGFKGIPWYHNOFFEVSESATVE
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International, Inc., 7300 NW
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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Zea mays mRNA for poly(ADP-ribose) polymerase (3211bp).
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Kushnir, S.
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DSDESLDDKYRKLHCDITPLAHDSEDYKLIEQYLLNTHAPTHKDWSLELEEVFSLDRD
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ESEFVKWRDDVVVPCGKPVPSSIRSBELMYNBYIVYNTSQVKMQFLLKVRFHHKR"

604 c 813 9 826 t 11; aagtcatgccggtccctatcgccaaggaccagctccgtcttggcaagatggttcaggcg 120 172 232 121 tcacagttcgacggcttcatgccgatgtggaaccatgccaggtgcatcttcagcaagaag 180 240 300 360 439 420 480 540 Gaps 499 559 619 9 009 619 099 739 720 780 799 859 840 919 979 cctgagaaatgtacaattgagattgctccatctgcccgtacttcatgtagacgatgcagt TCACAGTTCGACGCTTCATGCCGATGTGGAACCATGCCAG------aaccagataaaatccgttgacgatgttgaagggatagatgcacttagatgggatgatcaa gaaagattacaaaaggatcggtccgtcttcagctaagcttgagagtgaaggtcccaag GAAAAGATTACAAAAGGATCGGTCCGTCTTTCAGCTAAGCTTGAGGTGAAGGTCCCAAG aaaaaagatgttggcaacaatgaacaaaataagggttccaagcgcaagaaagtgaaaat gatattgatagctacaaatccgccaggttagatgaaagtacatctgaaggtacagtgcga aagticicaggcigggatactitgiccgatgaggataagagaaccatgcicgatctigti aagcttaaggagcaaagtgacacactttggaagttaaaggatggacttaagactcatgta toggotgotgaattaagggatatgcttgaggctaatgggcaggatacatcaggaccagaa 45; Length 3211; Indels 16; 8; DB 92.2%; Score 2720; Ellarity 97.2%; Pred. No. 0; Conservative 22; Mismatches Similarity ø Matches 2869; Query Match Local 173 61 233 181 320 380 274 241 440 301 361 481 541 620 680 661 740 721 800 860 601 781 841 BASE CO ORIGIN ö g Q ò õ g a

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parp-1
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  AJ131705.1 GI:4038490
NAD(+) ADP-ribosyltransferase;
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Arabidopsis thaliana mRNA for poly(ADP-ribose) polymerase.
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ILDANSSTELESLSGRRS IPDSDQEALLPUKKRALPARKTETARROPRSAGTKRUD
SUDNIS SKIAKSSPDNGTSCALDOPGSKEKERANDIKDDLKKYVYSABLREML
EVNENSTRAKSSELDLRDKCADGMMFGPLALCPMCSGHLSFSGGLYRCHGYISEWSKCSH
STLDPDRIKTKWRIPDETENDPLLKWRNSQKSYKRRILFWYLSGETSGGGGSBADTD
SSRSRELADLKYGANTRERQPWKR RIEBGABFHANVKGTSCIVVCGLTDIRDAE
MRKARRWYAIVREDYLLVDCFKKQRKLPFDKYKIEDTSBSLUTVKVKGRSAVHBASGL
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GGNKVEEMSKSDAVHEFKRLFLEKTGNTWESWEQKTNFQKQPGKFLPLDIDYGVNKQV
AKKEPFQISSNLAPSLIELMKMLFDVETYRSAMMEFEINMSEMPLGKLSKHNIQKGFE
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GKHSTKGLGKKVPQDSEFAKWRGDVTVPCGKPVSSKVKASELMYNEYIVYDTAQVKLQ
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Submitted (17-DEC-1998) Kazmaier M., Departement D'Ecophysiologie
Vegetale Et De Microbiologie, Commissariat A L'energie Atomique,
CEA Cadarache, Lab. De Radiobiol. Vegetale, Bat. 185, 13108 St.
Paul-les-Durance, FRANCE
                                                                                                      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
gene; poly(ADP-ribose)
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/EC_number="2.4.2.30"
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/protein_id="CAA10482.1"
/db_xref="G1:4038491"
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/cultivar="landsberg erecta"
/db_xref="taxon:3702"
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۾ ج	131	ACTCACTTCGATGGCATCATGCCCATGTGGGAACCATGTTGTATACTGAAGAGGCG	9
ъ a	181	aaccagataaaatccgttgacgatgttgaagggatagatgcacttagatggatg	240
^		gagaagatacgaaactacgttgggagtgctcagctggt	7
ڡ	<b>S</b>	CAAAAGATTAGAAAATATGTCGAAGCAGGGAGTAACACAAAGCACAAGCACAGGC	ā 6
<u>م</u> ح	311	acadetectadetectoctoctgagaargtacattgagatrgeteca acadecaggatrgeteca	330
.₹	331	tctgccgtacttcatgtagacgatgcagtgaaaagattacaaaaggatcggtccgtctt	390
۾	371	rgaaagaagatacgta	430
<u>ب</u> بخ	391	tcagctaagcttgagagtgaaggtcccaagggtataccatggtatcatgccaactgtttc	450
a >		getaggataetttgteega	, <del>,</del>
م ،	491		550
<u>~</u>	511	catgotogatottgttaaaaaagatgttggcaacaatgaacaaa	570
۵	551		610
y d	571	aagggttccaagcgcaagaaaagtgaaaatgatattgatagctacaaatccgccaggtta 	630
>	631	gatgaaagtacatctgaaggtacagtgcgaaacaaagggcaacttgtagacccacgtggt	069
ð	664	TTCTGTTGATAACGAGAAGTCGAAACTAGCAAAAAGTAGTTTTGACATGTCTACAAGTGG	723
<u>&gt;</u> 4	691	tocaatactagttcagctgatatccaactaaagcttaaggagcaaagtgacacactttgg	750
9 ≥	51	cttaaqactcatqtatcqqctqctqaattaaqqqatatqcttqa	
۾ .	00	GACCTGAAGGATGATGTGAAAAAATGTAAGATCAGCTGAGTTGCGGGAAATGTTGAA	4
<u>≻</u>	811	gctaatgggcaggatacatcaggaccagaaaggcacctattggatcgctgtgcggatgga	870
۵	842	GTAAATGAACAAAGTACAAGGATCTGAACTTGATCTGCGTGATAAATGTGCTGATGGC	901
<u>≯</u>	~	atgctatttggagcgctgggtccttgcccagtctgtgctaatggcatgtactattataat	m 1
ō	902	ATGATGTTTGGCCCACTCGCTCTCTGCCCAATGTGCTCTGGGCATCTTTCTT	o o
<u>ک</u> و	931	ggtcagtaccaatgcagtggtaatgtgtcagagtggtccaagtgtacatactctgccaca 	990
>	6	gaacctgtccgcgttaagaagaagtggcaaattccacatggaacaaagaatgattacctt	105
ą	1022		108
<u>&gt;</u> -	in	taagaaaccagagagggttcttccac 	Η.
۵	1082	CTGAAGTGGAATAAGTCTCAAAAGAGTGTGAAGCCAAAACGTATTCTGCGTCCTGTATTG	-i
٠ بج	1108	tcacctgagaaatctggaagtaaagcaactcagagaacatcattgctgtcttctaaaggg	$\overline{}$
ā	1142	TCTGGCGAGACATCTCAGGGTCAAGGTTCTAAAGATGCAACTGACTCCTCAAGGAGTGAA	120

1646 2247 tggcttcgatagcgacagtgatgaatctcttgatgataaatatatgaaacttcactgtga 2306 cattccttragratgggaaaagcatatacaatgcamccttaaacatgttctgacctgnca 1586 1766 aagataccaattgtaagggaggttacattggagaatgtgttaaaaga-acaaaatgctg 1406 1467 taaagttaagggccgaagtgcttgttcatyaagtcctcyggtttgcaagaatactgctca 1526 aaactcatgggaagcttgggaatgtaaaaccaattttcggaagcagcctgggagatttta 1826 1168 ttggataaattaaggttttctgttgtaggacaatcaaaagaagcagcaaatgagtggatt 1227 1202 AGGCTAGCAGATCTTAAAGTTTCAATTGCTGGAAATACTAAGGAAAGGCAACCATGGAAG 1261 1322 TTGGTTGTTGTGGACTGACAGATATCAGAGGCGCTGAAATGAGAAAGGCAAGGAGGATG 1381 1288 ttaattgcatgtggtgagctcgacaatgaaaatgctgaagtcaggaaagcaaggaggctg 1382 AAAGTGGCAATCGTGAGAGGATTATTTGGTTGATTGTTTTAAAAAACAGAGGAAACTT 1492 TAAAGTAAAAGGACGAAGGGCT--GTGCATGAAGCGTCTGGACGCTCCAAGAGCATG--TC 1587 cnaggtgtgyacaggctactatgtactccagatcattgaacaggatgatgggtctgagtg ggagatgtcaaaaactgaggcaatcaaggaattcaaaagattatttcttgagaagactgg 2067 aggacaccgctnatcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmat --GACTGAAAGCGACCCCCAGCCTACTATGAAAGAAAGCTTGTTGATGATGGTAAC 1348 1707 1527 1767 qq δλ Dp δy Op QY Db ò qq Qy qq Qγ QQ óγ Op QY Db Ωý Op QΥ QQ ò qq δλ qq δλ g δy qq οy q δ g οy g ŏ

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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 3036)
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Ittel,M.E., Garnier,J.M., Jeltsch,J.M. and Niedergang,C.P. Chicken poly(ADP-ribose) synthetase: complete deduced amino acid sequence and comparison with mammalian enzyme sequences Gene 102 (2), 157-164 (1991)
2486
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                                                                                                                                                                                                                                                 attatggcacggttcaaggttgacgaattttgtgggaattcttagtcaagggctaagaat 2546
                                                                                                                                                                                                                                                                                                                                    2560 TGCACCTCCAGAAGCTCCTGCTACTGGTTACATGTTTGGAAAAGGGATATACTTTGCTGA 2619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2787 agagittgigaagiggaggatgatgicgiagitccigcggcaagccggtgccatcaic 2846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPADPRP 3036 bp mRNA VRT 12-SEP-1993 Chicken mRNA for poly(ADP-ribose) polymerase (EC 2.4.2.30). X52690
                                                                              TATCTCACCACTTCCTCATGATAGCGAAGATTATCGATTAATCGAGAAGTATCTTAACAC
                                                                                                                                   2427 tcgagatggagaacttaataagtactcaagatataaaaaataatctgcataacaagatgct
                                                                                                                                                                                                                                                                                                                                                                                  2607 tctagtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgat
                                                                                                                                                                                                                                                                                                                                                                                                   cacacatgctcctactcacaaggactggtcgctggaactggaggaagtttttcacttga
                                                                                                                                                                                                   2500 CCTATGGCATGGTTCTCGATTAACGAATTTTGTTGGAATATTGAACCAAGGACTGAGAAT
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AKKKSKKEKEKESKOEKOLKEOTELIMGIKDELRKUCSTNDIKELLIANKOEVPSGEN
ALIDRYADGAREGALLDCEEKGGYPKSDAYYCGSTNDIKELLIANKOEVPSGEN
ALIDRYADGAREGALLDCEEKGGYPKSBAYYCGSDITAMYKCVAKTOPRIKDWYI
PREFREI PYLKKFKCKODR IFPPEAATVNGAPPPPRAAPLITETYTAPODKPLTINMKI
LITLGKLSKNKEEVKNIVVELGGKMTTTANKATLCISTOKEVEKMSKKMEEVKDAKVY
VSEEFLKDYKS GSNKGPOLLISHAISPWGARVTEHDEWAYDGKCSKFAMEVKDAKVY
EEQQESKSEKKMKLIVYGGAAVDPDSGLEDSAHVFENGGKIFSATLGIVDINKGGTNSY
YKLOLLEDDRESSKYWPRSWGRYGTVIGSNK LÖQMPSKEDAVBFRIGGY IFSATLGIVDINGENST
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WEFEIDLÓKNELGKUSKRÓ 10SAYS ILNEVQDASVBOGGSESOLIDLENRFYTLIPHD
FGMKRPPLLSNLEY IQAKVQMLDNLLDIEVAYSLLRGGNEDGDRDPIDINYEKLRTDI
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                                                                                                                                                                                                                                                                                                                                VGKAEKSLTDFAAAEYAKSNRSTCKGCEQKIEKGQIRISKKMVHPEKPQLGMIDNWYHP
DCFVSRRAELGFLPAYGATQLLGFSILKAEDKETLKKQLPATKTEGKRKGEEVDGNVV
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LILLGEVALCHMYELKNASHITKLPKOKHSVKGLGKTARDPTATTLDGVEVPLGNGI
STGINDTCLLYNEXIVYDAVNKYLLKLKFNYKTSLM"
631 c 818 q 651 t
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                                                                                                                                  /note="Poly (ADP-ribose)polymerase (AA 1-1011)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.5%; Score 249.4; DB 5; Length 3036; 52.4%; Pred. No. 3.1e-53; tive 10; Mismatches 593; Indels 43;
                                                                                                                                                                                                                                              /db_xref="SWISS-PROT:P26446"
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                                                                                                                                                                                       /protein_id="CAA36917.1"
/db_xref="G1:63743"
                                                                              /tissue_type="oviduct"
                                                 /db_xref="taxon:9031
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Bovidae; Bovinae; Bos
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2212 CCTCATGACTTTGGGATGAAGAAACCACCTCTTCTCTCAGTAACTTGGAATACATTCAGGCT 2271
                                                                                                                                                                                                                                                                                                                                                                                                        2488 ttatggcacggttcaaggttgacgaattttgtgggaattcttagtcaagggctaagaatt 2547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2689 ATGGTTTCCAAGAGTGCCAACTACTGTCACATCTCAAGCTGATCCAATTGGGTTAATA 2748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2866 ACAGCCACTACAACCCTTGAFGGTGTAGAAGTTCCCTTAGGGAATGGGATCTCAACAGGA 2925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2926 ATTAMTGATACTTGTCTGCTGTACAATGAATATATTGTGTATGATGTTGCTCAGGTAAAT 2985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA binding protein; helix-turn-helix; nuclear location signal; poly(ADP-ribose) synthetase; zinc-binding finger motif. Bovine thymus, cDNA to mRNA, clone pSO-7.
                                                          atcaccccgctggctcacgatagtgaagattacaagttaattgagcagtatctcctcaac 2367
                                                                                                                                                                                                                                                                                                                                                                                   cgagatggagaacttaataagtactcaagatataaaaataatctgcataacaagatgcta 2487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTGGCACGGTTCCCGCACCCAACTTCGCTGGTATCCTCTCACAGGGTCTCCGGATA 2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcacctcctgaggcacctgttactggctatatgttcggcaaaggcctctactttgcagat 2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2629 GCTCCCCCTGAAGCTCCTGTGACCGGCTACATGTTTGGGAAGGGCATCTACTTTCGAGAT 2688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctagtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatg 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2749 CTACTGGGAGAAGTTGCCCTCGGAAATATGTATGAGCTAAAGAATGCTTCTCACATAACA 2808
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                                                                                                  2272 AAAGTGCAGATGTTGGACAACTTGCTCGATATTGAGGTTGCTTACAGTCTTCTCAGAGGT 2331
                                                                                                                                         ggettegatagegaeagtgatgaatetettgatgataaatatatgaaaettcaettgtgae 2307
                                                                                                                                                                                 2332 GGAAATGAAGATGGAGACAAAGACCCAATTGATATCAATTATGAAAAGCTCCGAACTGAT 2391
                                                                                                                                                                                                                                                            2392 ATTAAGGTGGTTGACAAAGATTCAGAAGAAGCCAAGATTATTAAACAATACGTGAAAAAT 2451
                                                                                                                                                                                                                                                                                                    acacatgotoctactcacaaggactggtcgctggaactggaggaagttttttcacttgat 2427
                                                                                                                                                                                                                                                                                                                                         2452 ACTCATGCTGCTACTCACAATGCATATGACCTCAAAGTTGTGGAAATCTTCAGGATTGAA 2511
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Cloning of a full-length cDNA encoding bovine thymus
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ANTRYSEDECODISSTRAINGELISTHILSEWGAEWWVEPPEAVGEKGSGAAPSK
SKGPVKEEGTNKSEKRMKLTLKGGAAVDPDSGLEHNAHVLEKGGKVFSATGLVDIVK
GTNSYKLQLLEDDKESKYWIFRSWGRYGTVIGSNKLEOWESKEDALEHYKLYEEKT
GNAMHSKNFTKHPKKFYPLEIDYGODEBAVKLLYVPGTKSRLPKPYONLIKMIFDVE
SWKRAWYEYEIDLOKODEBANKILYVPGTKSRLPKPYONLIKMIFDVE
SWKRAWYEYEIDLOKOREKLSKROIOAAYSTLSEVQOALSOGSSBDAILDLISNRFYT
LIPHDFGMKRPPLLINNANSVQAKVEMLDNLLDIEVAYSLLRGGSDDSSKDFILDLISNRFYT
KTDIKVYNDSBEBAEITRYVWNTHATTHNAN DIEVVDIFK IEREBEGSDRSKRPFROL
HNRLLMHGSRFTNFAGILSOGLRIAPPEAPVTGYNFGKGYTFADPSSSRYKPFKOL
FOPIGLILLGEBALGNWYELKHARISKLPKGKHSVKGLKTTPDPSASITVDGVEVP
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IDEVTKKKSKKEKDKEILGFRATKAQNDLTANVKDELKKAGSTNDLKEILTFRKQEDY
SEGSALLDRYADGMYGFALLFDEEGGGQLFKKGDBYVCTGDVTAMTKCMVTQTPNRK
SWYTPKEFREISYFKLKIKKQDRIFPPESSTPVGAAAPSAASABANHSGPDKPL
SMMKILTLGKLSQNKDEVKATIEKLGGKLTGTANKASLCISTKKEVDKINKKMEEVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="Baal4114.1"
| Dacksid="G1:217582"
| /translation="MarsSSDSL"
| DGKIPHWYHLSCFWKVGFSIWHPDVEVEGFSELRWDDQQTIKKMAETGGRTDVSGKGQ
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                                                                                                                                                                                                                                                                                                                                                                                               Zinc-binding finger motifs are observed in seq. 21-51 and 128-165. The sequences, 200-220 and 250-270, showed helix-turn-helix structure. Nucleotide-binding fold was found in seq. 890-903. Location/Qualifiers
poly(ADP-ribose) synthetase: evolutionally conserved segments and their potential functions
                                                                                                                                                                       Department of Clinical Science and Laboratory Medicine Faculty of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1587 cnaggigitgyacaggctactatgiactccagaicaitgaacaggaigaiggictgagig 1646
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                                                                                                                                                                                                          Medicine, Kyoto University
Shogoinkawahara-cho 54, Sakyo-ku
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These data kindly submitted
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                                                                                                                                                                                                                                                              2121 agcmatssytttttcactcttatcccttctattcatcctcatattatacgggatgaggat 2180
                                                                                                                                                                                                                                                                                                                                  2181 gatttcatattcaaaggcgaaaatgcttgaagctctgcaggatattgaaattgcttcaaa 2240
                                                                                                                                                                                                                                                                                                                                                       2241 gata----gttggcttcgatagcgacagtgatgaatctcttgatgataaatatatgaa 2294
                                                                                                                                                                                                                                                                                                                                                                                                                                        2410 TCTACTTAGGGGTGGTTCTGATGACAGCAGGACCCCATTGATGTCAACTATGAGAA 2469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2295 acttcactgtgacatcacccgctggctcacgatagtgaagattacaagttaattgagca 2354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2355 gtatotoctcaacacatgctcctactcacaaggactggtcgctggaactggaggaagt 2414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2887 TCGACATATCAGCAAGTTACCCAAGGGCAAGCACACGTGTCAAAGGTTTAGGCAAAAC--- 2943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2944 TACCCCTGACCCATCGCTAGTATTACTGTGGATGGTGGGAGGTGCCTCTCGGGACAGG 3003
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2059 IGGCACCAAGTCCAAGCCCCAAGCCAGCAGAACTCATTAAGATGATCTTTGATGT 2118
                                                                                                                    2001 gaagctaagcmaggraaatattgagraaggatttgaagcattaactkrgrtacmgrattt 2060
                                                                                                                                                                                                                            -----GCACTGTCCCAGGGCAGCAGTGACTCTCACATCCTGGATCTCTCCAACCGCTT 2289
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                                                                                                                                                  2179 GAAGCTGAGCAAAAGGCAGATCCAGGCTGCATACTCCATCCTCAGTGAGGTCCAGCAG--
                                                                        2061 atttgaaggacaccgctnatcaagcactggcttgttrgagaaagctnaattgttgytgsg
                                                                                                                                                                                                                                                                                               2290 CTACACCCTGATCCCCCACGACTTCGGGATGAAGAAGCCCCCGCTGCTGAACAACGCAAA
                                                     1941 ggagacatatagagctgctatgatggaatttgaaawtaatatgtcagaaatgcctcttgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2895 atcccaggtgaagatgcagttcttgctgaaggtgcgttccatcacaaga 2944
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                                                                                                                                                                                                                                                                                                                                                                                                                          Isolation of the poly(ADP-ribose) polymerase-encoding cDNA from Xenopus laevis: phylogenetic conservation of the functional domains Gene 137 (2), 293-297 (1993) 94131300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation of Poly(ADP-ribose) Polymerase cDNAs from Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 3718)
Uchida,K., Uchida,M., Hanai,S., Ishikawa,K., Ozawa,Y., Ueno,N. and
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3718)
Uchida,K., Uchida,M., Hanai,S., Ozawa,Y., Ami,Y., Kushida,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1847 CTGGGGTCGGGTGGGCACAGTAATAGGCAGAAAAGCTAGAAGAAGATGTCTTCCAAGGA 1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1602 ctactatgtactccagatcattgaacaggatgatgggtctgagtgctacgtatttcgtaa 1661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1722 tgaggcaatcaaggaattcaaaagattatttcttgagaagactggaaactcatgggaagc 1781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Cherry Salmon using heterologous oligonucleotide consensus sequences: gene conservation in amphibia, fish, and insect Unpublished (1993)
Submitted (15-MaR-1993) to DDBJ by:
Kazuhiko Uchida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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04-FEB-1999
                                                                                                Xenopus laevis egg, oocytes, germ cell, cDNA to mRNA, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3718;
Frog mRNA for poly(ADP-ribose) polymerase. D14667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.1%; Score 239.2; DB 5; Best Local Similarity 51.8%; Pred. No. 1.3e-50; Matches 701; Conservative 12; Mismatches 602;
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Institute of Basic Medical Sciences
University of Tsukuba
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kzuchida@md.tsukuba.ac.jp
0298-53-3039.
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1. .3718
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1. .3718
                                                                                    poly (ADP-ribose) polymerase.
                                                                                                                                                                                                     Xenopodinae; Xenopus.
1 (bases 1 to 3718)
Uchida, K.
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COMMENT
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AUTHORS
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1967 GC------CCAATTTCACCAAATACCCCAAAAAATTCTATCCCCTGGAAATAGA 2014 1896 tcttgctcctcaattgctagaactcatgaagatgcttttcaatgtggagacatatagagc 1955 2136 actottatocottotattoatoctoatattataogggatgaggatgatttoatattoaaa 2195 99cgaaaatgcttgaagctctgcaggatattgaaattgcttcaa----agatagttgg 2249 2076 ctnatcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmatssyttttc 2135 2252 CTTAAGCGAAGCCCGATTACTGGATCTCTCCAATCAGTTTTACACACTCATACCTCATGA 2311 2312 TTTTGGAATGAAGAAGCCCCCGCTGCTAAATAACCTAGAGTACAT-----ACAGGCTAA 2365 2366 AGTGCAGATGCTGGATAATCTGCTCGACATTGAAGTTGCTTACAGCCTGTTGAGAGGTGG 2425 2250 cttcgatagcgacagtgatgaatctcttgatgataaatatatgaaacttcactgtgacat 2309 2429 2662 2549 2546 GCACGCTGATACGCACAATGCATATGATCTTGAGGTCCTCGAGATATTCAAAATCGACCG 2605 2430 agatggagaacttaataagtactcaagatataaaaaataatctgcataacaagatgctatt 2489 2722 2610 agtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatgct 2669 2843 ACTGGGGGAGGTGGCCCTCGGAAACATGCATGAGCTGAAAGCAGCATCACAAATTACAAA 2902 acctccaagagggaagcattcgaccaagggattaggcaaaaccgtgccactggagtcaga 2789 gtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccggtgccatcatcaat 2849 2963 TACTGTACA---GCTGGATGGAGGGATGTTCCTCGGGAAAGGAACTTCTGCAAATAT 3019 1782 ttgggaatgtaaaaccaattttcggaagcagcctgggagattttacccacttgatgttga 2015 CTATGGACAGGAAGAAGATGTGGTGAAGAAGCTCTCAGTGGGGGGCCGGCACAAAATCCAA 2075 GCTCGCTAAGCCTGTCCAGGAACTGATCAAATTAATTTTTGATGTGGAGAGCATGAAAAA 1956 tgctatgatggaatttgaaawtaatatgtcagaaatgcctcttgggaagctaagcmaggr 2016 aaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccg 2426 CGCCGATGATGGTGAAAGGATCCCATTGATGTGAAATATGAAAGATTAAGACTGACAT 2310 cacccgctggctcacgatagtgaagattacaagttaattgagcagtatctcctcaacac 2370 acatgctcctactcacaaggactggtcgctggaactggaggaagttttttcacttgatcg 2606 TGAAGGTGAATATCAGCGGTATAAACCATTTAAA----CAGCTACAAACGCCAGCTGCT 2670 tctttctgaggttgctttaggagacatgtatgaactaaaggaaagccacgtccatggacaa 2196 g ò Q a q ò 셤 ô ò οχ g g ò ò 셤 à g ò q ŏ g ò g g à ò g ò qq ò a ò

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Direct Submission
Submitted (15-MAY-1992) Saulier-le Drean B.M., Lab. de Biol. et
Genet. du Developpement, Universite de Rennes I. URA CNRS 256,
Campus de Beaulieu, Av. du Gal LeClerc, Rennes-cedex, FRANCE, 35042
1. 3617
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YAKSNRSACKGCEQKIEKGQIRISKKSVDVERPQLGMIDRWYHPDCFVSSREELDFLB
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KFKRHDRAFPPCAAPTPISPPAAPEFKPTVEETFPEGKPLINTKVLLIGKLSKNKDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="poly ADP-ribosylation, DNA repair"
//functern sequence is in conflict with the conceptual
translation; poly(ADP-ribose) polymerase"
/citation=[1]
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KLSKRQIQSAYSILSQVQQAVSESLSEARLLDLSNQFYTLIPHDFGMKKPPLLNNLEY
IQAKVQMLDNLLDIEVAYSLLRGGADDGEKDPIDVKYEKIKTDIKVVAKDSEESRIIC
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SQGLRIAPPBAPVTGYMFGKGIYFADMYSKSANYCHAMPGSPIGLILLGEVALGNMHE
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TVKGGAAIDPDSELEDSCHVLETGGKIFSATLGLVDITRGTNSYYKLQLIEHDRDSRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. et Genet. du Developpement, Universite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                 /clone_lib="oligo dT primed lambda gt10 library of D.
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2850 taggagototgaactoatgtacaatgagtacatogtotacaacacatocoaggtgaagat
                                                                                                                                                                                                                                                                                                             X.laevis PARP gene encoding poly(ADP:ribose) polymerase 212139
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                                                                                                    2910 gcagttcttgctgaaggtgcgtttccatcacaag 2943
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                                                                                                                                                                                                                                                                                                                                                                  212139.1 GI:64967
poly(ADP-ribose) polymerase.
African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus.

1 (bases 1 to 3617)
Saulier-le Drean, B.M.
Thesis (1992) Lab. de Biol.
de Rennes I. URA CNRS 256
2 (bases 1 to 3617)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2076 ctnatcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmatssyttttc 2135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2292 CGCCGATGATGGTGAAAAGGATCCCATTGATGTGAAATATGAAAAGATTAAGACTGACAT 2351
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                                                                                                                                                                                                                                                                                                                                1713 CTGGGGTCGGGTGGGCACAGTAATAGGCAGTAAAAAGCTAGAAGAGATGTCTTCCAAGGA 1772
                                                                                                                                                                                                                                                                                                                                                                     1722 igaggcaaicaaggaaitcaaaagaitaitittigagaagaciggaaacicaigggaagc 1781
                                                                                                                                                                                                                            1602 ctactatgtactccagatcattgaacaggatgatgggtctgagtgctacgtatttcgtaa 1661
                                                                                                                                                                                                                                                           1653 CTATTATAAGCTGCAACTTATAGAGCACGACAGAGATTCCAGGTACTGGGTGTTCCGATC 1712
                                                                                                                                                                                                                                                                                                 1662 gtggggacgggttggggggtgagaaattggagggcaaaaactggaggagatgtcaaaaac 1721
                                                                                                                                                      Ouery Match

8.1%; Score 238.2; DB 5; Length 3617;

Best Local Similarity 51.7%; Pred. No. 2.4e-50;

Matches 700; Conservative 12; Mismatches 602; Indels 39;
                    IVYDIAQVNLKYLLKLKFNYKGGMMW"
                                                                                        819
                                                                                       910 g
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3551. .3556
3574
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3640)
Uchida, K., Morita, T., Sato, T., Ogura, T., Yamashita, R., Noguchi, S., Suzuki, H., Nyunoya, H., Miwa, M. and Sugimura, T.
Nucleotida sequence of a full-length cDNA for human fibroblast poly(ADP-ribose) polymerase
Biochem. Biophys. Res. Commun. 148 (2), 617-622 (1987)
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                                                                                                                                                                                                                                                                                                            2610 agtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatgct 2669
                                                                                                                                                                                                                                                           2649 GGTATCCAAAAGTGCAAACTACTGTCATGCAATGCCGGGTAGCCCCATAGGGCTGATCTT 2708
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2490 atggcacggttcaaggttgacgaattttgtgggaattcttagtcaagggctaagaattgc 2549
                                                 2529 TIGGCACGCTCCCGCACCACAAATTTTGCAGGAATATTGTCTCAGGGTCTCCGAATTGC 2588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2790 gtttgtgaagtggagggatgatgtcgtagttccctgcggcaagccggtgccatcaat
                                                                                                       2550 acctcctgaggcacctgttactggctatatgttcggcaaaggcctctactttgcagatct
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/db_xref="GDB:G00-119-508"
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/organism="Homo sapiens"
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/gene="PPOL"
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SAILDRVANGGMYFGALLPCEECSGGLVFKSDAYYCTGDVTAMTKCWYKTOPPNRKEWY
TPREFREIS YLKKLKYKKODRIFPPETSASVAATPPPSTASAPAAVNSSASADKPLSN
MKILTLGKLSRNKDEWRANIEKLGGKLTGTANKASLCISTKKEVEKNNKKMEEVKRAN
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Chromosome 1p11-qter. 999 a BASE COUNT ORIGIN

7; 1602 ctactatgtactccagatcattgaacaggatgatgggtctgagtgctacgtatttcgtaa 1661 1843 CTACTACAAGCTGCAGCTTCTGGAGGACGACAAGGAAAACAGGTATTGGATATTCAGGTC 1902 1903 cresseccerereseracerearcesraceaacaaacresaacadarecegrecaasa 1962 2023 C------AAAAATTTCACGAAGTATCCCAAAAAGTTCTACCCCTGGAGATTGA 2070 1662 gigggacgggitgggagigagaaaaitggagggcaaaaaciggaggagatgicaaaaac 1721 1722 tgaggcaatcaaggaattcaaaagattatttettgagaagaetggaaactcatgggaagc 1781 1782 ttgggaatgtaaaaccaattttcggaagcagcctgggagattttacccacttgatgttga 1841 2075 1896 tcttgctcctcaattgctagaactcatgaagatgcttttcaatgtggagacatatagagc 1955 2131 GCTCCCCAAGCCAGTTCAGGACCTCATCAAGATGATCTTTGATGTGGAAAGTATGAAGAA 2190 2191 AGCCATGGTGGAGTATGAGATCGACCTTCAGAAGATGCCCTTGGGGAAGCTGAGCAAAAG 2250 2305 2421 2196 ggcgaaaatgcttgaagctctgcaggatattgaaattgcttcaa----agatagttgg 2249 2250 cttogatagogacagtgatgaatctttgatgataaatatatgaaacttcactgtgacat 2309 2310 cacccogctggctcacgatagtgaagattacaagttaattgagcagtatctcctcaacac 2369 Gaps 1963 GGATGCCATTGAGGACTTCATGAATTATATGAAGAAAAAACCGGGAACGCTTGGCACTC 1956 tgctatgatggaatttgaaawtaatatgtcagaaatgcctcttgggaagctaagcmaggr 2251 GCAGATCCAGGCCGCATACTCCATCCTCAGTGAGGTCCAGCAGGGGGGT-----GTCTCAG 2016 aaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccg 2076 ctnatcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmatssytttttc 2306 GGCAGCAGCGACTCTCAGATCCTGGATCTCTCAAATCGCTTTTACACCCTGATCCCCCAC 2136 actottatocottotattoatoctoatattataogggatgaggatgatttoatattoaaa 2366 GACTTTGGGATGAAGAAGCCTCCTCGAACAATGCAGA----CAGTGTGCAGGCCAA Query Match 7.6%; Score 224.6; DB 9; Length 3640; Best Local Similarity 51.1%; Pred. No. 7.8e-47; Matches 693; Conservative 11; Mismatches 612; Indels 39; ð ò g ò Q õ g ò g Op 6 g õ ô g à g ò a à g ŏ g

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GCFVKNREELGFRPEYSASQLKGFSLLATEDKEALKKQLPGVKSEGKRKGDKVDEV
VAKKKSKKEKDKDSKLEKRLKAQNDLIWNIKDELKKVCSTNDLKELLIFNKQQVPSGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSKAEKTLGDFAAEYAKSNRSTCKGCMEKIEKGOVRLSKKMVDPEKPQLGMIDRWYHP
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TPKEFREISYLKKLKVKKQDRIFPPETSASVAHPPFSTASAPAAVNSSASADKPLSKM
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                                                                               2430 agatggagaacttaataagtactcaagatataaaaataatctgcataacaagatgctatt 2489
                                                                                                                                                                atggcacggttcaaggttgacgaattttgtggggaattcttagtcaagggctaagaattgc 2549
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2370 acatgctcctactcacaaggactggtcgctggaactggaggaagttttttcacttgatcg
                       2662 TGAAGGCGAATGCCAGCGTTACAAGCCCTTT---AAGCAGCTTCATAACCGAAGATTGCT
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Buerkle,A., Zur,H.H. and Kuepper,J.
VECTORS AND VIRUSES FOR USE IN GENE THERAPY
Patent: WO 9618737-A 1 20-JUN-1996;
DEUTSCHES KREBSFORSCH (DE)
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/db_xref="taxon:32644"
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Location/Qualifiers
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WHSKNFTKYPKKFYPLEIDVGQDEBAYKKLYVNPGTKSKLPRPVDLIKMIFDVESMK
WANDYEIDLOKMPLGKLESKOIQAAPSILSEVQOAVSGGSSDSQILDLSNRFYTLIP
HDFGMKRPPLLNNADSVQAKTBALDNILDIEVAYSLLRGGSDDSSKDPIDVNFKKTIP
DIKVVDRDSEEAEIIRKYVKNTHATTHNAYDLEVIDIFKIERGGSDGSKRPFVQLNR
                                                                                                                                                       RLLWHGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHTSQGDP
IGLILLGEVALGNMYELKHASHISKLPKGKHSVKGLGKTTPDPSANISLDGVDVPLGT
GISSGVNDTSLLYNEYIVYDIAQVNLKYLLKLKFNFKTSLW"
RVVSEDFLQDVSASTKSLQELFLAHILSPWGAEVKAEPVEVVAPRGKSGAALSKKSKG
QVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHSAHVLEKGGKVFSATLGLVDIVKGTN
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                                                                                                                                                                                                                                                                                                                  7.6%; Score 224.6; DB 6; Length 3792; 51.1%; Pred. No. 7.8e-47; rative 11; Mismatches 612; Indels 39;
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Draft entry and printed copy of sequence for [1] kindly provided by Y.Shizuta, 23-NOV-1987.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3795)
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2555 TCATGCAACCACACACAATGCGTATGACTTGGAAGTCATCGATATCTTTAAGATAGAGCG 2614
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Human poly(ADP-ribose) synthetase MRNA, complete cds.
J03473
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Human placenta, cDNA to mRNA (library of H.Okayama), clones
pPARS[1,11,21,32,32,41,-F].
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Matsuda,Y., Katunuma,N., Kangawa,K., Matsuo,H., Hirose,T.,
Inayama,S. and Shizuta,Y.
                                                                                                                                                                                                                        2430 agatggagaacttaataagtactcaagatataaaaaataatctgcataacaagatgctatt
                                                                                                                      2490 atggcacggttcaaggttgacgaattttgtggggaattcttagtcaagggctaagaattgc
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                                                                            2615 TGAAGGCGAATGCCAGCGTTACAAGCCCTTT---AAGCAGCTTCATAACCGAAGATTGCT
                                                                                                                                                          2672 GIGGCACGGGICCAGGACCACCATITGCIGGGATCCIGICCCAGGGICTICGGATAGC
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/note="poly(ADP-ribose) synthetase"
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J. Biol. Chem. 262 (33), 15990-15997 (1987)
88058958
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/db_xref="taxon:9606"
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TALDRVADGOVYGALLEGEGSGQLYKSDAYYGTGDVTAMTKCWYKTOTPBYREWY
TALDRYADGOVYGALLEGEGSGGLYGFSDAYATOTBOYTAMTKGWYKTOTPBYREWY
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MKILTLGKLSRNKDEVKAMIEKLGGKLTGTANKASLCISTKREVEKNNKKMEEVKEN
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GCFVKRNREELGFRPEYSASQLKGFSLLATEDKEALKKOLPGVKSEGKRKGDKVOGVDE
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KKAMVEYEIDLQKMPLGKLSKRQIQAAYSILSEVQQAVSQGSSDSQILDLSNRFYTLI
PHDFGMKKPPLLNNADSVQAKVEMLDNLLDIEVAYSLLRGGSDDSSKDPIDVNYEKLK
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PIGLILLGEVALGNMYELKHASHISKLPKGKHSVKGLGKTTPDPSANISLDGVDVPLG
TGISSGVNDTSLLYNEYIVYDIAQVNLKYLLKLKFNFKTSLW"
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/db_xref="GDB:G00-119-508"
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                  /protein_id="AAB59447.1"
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2262 GGCAGCACTCTCAGATCCTGGATCTCTCAAATCGCTTTTACACCCTGATCCCCCAC 2321
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                                                                               actettatecettetatteateeteatattataegggatgaggatgattteatatteaaa
                                                                                                                                                                                                                    2378 GGTGGAAATGCTTGACAACCTGCTGGACATCGAGGTGGCCTACAGTCTGCTCAGGGGAGG
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                                                                                                                                     GACTTTGGGATGAAGAAGCCTCCGCTCCTGAACAATGCAGA - - - - CAGTGTGCAGGCCAA
                                                                                                                                                                                             ggcgaaaatgcttgaagctctgcaggatattgaaattgcttcaa----agatagttgg
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; mammalia; Eutheria; Primetes; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1320; 1560 to 1771)
Suzuki, H., Uchida, K., Shima, H., Sato, T., Okamoto, T., Kimura, T. and

Human placenta cDNA to mRNA, clone lambda-PAP803.

Homo sapiens

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VKAEPVEVVAPRGKSGAALSKKSKGQVKEEGINKSEKRMKLTLKGGAAVDPDSGLEHS
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YDIDFKIEREECORYKPROCHNRELMGGSRTPRAGISGGELRIAPEAPVTGYM
PGRGIYFADNVSKANYCHTSQGPPGLILLGEVALGNMYELKHASHISKLPGKRKBY
RGGIKTTPDPSANISLDGVDVPLGTGISSGVNDFSLLYNEYIVYDIAQVNLKYLLKLK
Molecular cloning of cDNA for human poly(ADP-ribose) polymerase and
expression of its gene during HL-60 cell differentiation [published
erratum appears in Biochem Biophys Res Commun 1987 Nov
13;148(3):1549]
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QQAVSQGSSDSQILDLSNRFYTLIPHDFGMKKPPLLNNADSVQAKVEMLDNLLDIEVA
                                                                                                   2 (bases 1321 to 1559)
Suzuki,H., Uchida,K., Shima,H., Sato,T., Okamoto,T., Kimura,T. and
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                                                                   Biochem. Biophys. Res. Commun. 146 (2), 403-409 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 7.6%; Score 223; DB 9; Length 1771; Local Similarity 51.1%; Pred. No. 1.9e-46; nes 692; Conservative 11; Mismatches 613; Indels 3
                                                                                                                                                                       Biophys. Res. Commun. 148, 1549-1550 (1987)
                                                                                                                                                                                                                                                                                                                                                  /note="poly(ADP-ribose) polymerase"
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/protein_id="AAA51599.1"
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                                                                                                                                                                                                                        /organism="Homo sapiens"
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Cricetulus griseus poly ADP-ribose polymerase (PARP) mRNA, complete
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GGKSEKTLGDFAAEYAKSNRSTCKGCMEKIEKGQVRLSKKMLDPEKPQLGMIDRWYHP
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Cricetulus griseus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                      Ganesh, A.N., Phillips, E., Shah, R., Affar, E.B., Poirer, G., Thacker, J. and Meuth, M.

Suppression of hamster irsl and irs2 strains selected for resistance to 3 aminobenzamide
                                                                                                                                                                                                                                                                                                                                                                Utah,
                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae
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                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (14-JUL-1999) Oncological Sciences, University of
15 N. 2030 E., Salt Lake City, UT 84112, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3047;
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//translation="MKLTLKGGAAVDPDSGLEHSAHVLEKGGKVFSATLGIVDIVKGT
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XSY KLQLLESDKRESRYWIFRSWGRVGTVIGSNKLEOMPSKEDAVEHFMKLYEEKTGN
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                                                                                                                                                                                                            Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Submitted (23-MAR-1992) F. Potvin, Molecular Endocrinology, CHUL
                                                                           RNDARP2 1939 bp DNA ROD 20-MAY-1992
R.norvegicus mRNA for poly(ADP-ribose) polymerase (clone pRATC).
X65497
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                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/protein_id="CAA46478.1"
/db_xref="GI:56850"
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2994 GARATACCTGCTGARACTGARGTTTAATTTTAAGA 3028
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/tissue_type="prostrate"
/clone_lib="lambda EMBL4"
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/db_xref="taxon:10116"
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/EC_number="2.4.2.30"
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349 GAAAAACTTCACAAAGTATCCCCAAGAAGTTCCACCC----TCTGGCGATTGACTAIGG 402
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PIGLILLGEVALGNMYELKHASHISRLPKGKHSVKGLGKTTPDPSANISLDGVDVPLG
TGISSGVIDTSLLYNEYIVYDIAQVNLKYLLKIKFNEKTSLW"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3045)
6 Christenson, E., Demagqio, A.J., Goldman, P.S. and Mcelligott, D.L.
Human poly(adp-ribose) polymerase 2 materials and methods
TCOS CORPORATION (US)
1764 CTGGGGCCGTGTGGGTACGGTGGTAGCAACAAACTGGAACAGGATGCCGTCCAAGGA 1823
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Sequence 24 from Patent W00077179.
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/db_xref="GI:12310801"
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/db_xref="taxon:9606"
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                                                                                                                                                      1932 CTATGGCCAGGATGAAGAGGCAGTGAAGAAGCTCACAGTAAATCCTGGCACCAAGTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2016 aaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccg
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                                                                                                                                                                                                                                                                                                                                                                                                        2052 AGCCATGGTGGAGTATGAGATCGACCTTCAGAAGATGCCCTTGGGGAAGCTGAGCAAAAG
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/ TEARS TALE TODILADAQUIVA WARTEN TODICAND WARTEN WARTEN TO WARTEN TO WARTEN 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2937 GATAGACACCTCTCTACTATATAACGAGTACATTGTCTATGATATTGCTCAGGTAAATCT 2996
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Christenson,E., Demaggio,A.J., Goldman,P.S. and Mcelligott,D.L.
Tankyrase2 materials and methods
Patent: WO 0100849-A 136 04-JAN-2001;
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                                                              2910 gcagttcttgctgaaggtgcgtttccatcacaaga 2944
                                                                                                         2997 GAAGTATCTGCTGAAACTGAAATTCAATTTTAAGA 3031
                                                                                                                                                                                                                                                                 AX062277 3045 bp DNA
Sequence 136 from Patent WO0100849.
AX062277
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                                                                                                                                                                                                                                          2016 aaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccg 2075
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1932 CTATGGCCAGGATGAAGAGGCAGTGAAGAGCTCACAGTAAATCCTGGCACCAAGTCCAA 1991
                                                                                                          2052 AGCCATGGTGGAGTATGAGATCGACCTTCAGAAGATGCCCTTGGGGGAAGCTGAGCAAAAG 2111
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Search completed: March 7, 2002, 16:48:39 Job time: 8149 sec

Human brain poly-A Human ORFX ORF2673 Human cDNA sequenc

AAH14941

Human brain PARP2

3' end fragment of 5.3 kb EcoRI fragm

Poly(ADP-ribose)-p Poly(ADP-ribose)-p Oligonuclectide Dl Oligonuclectide Dl Oligonuclectide Dl Oligonuclectide D2 Oligonuclectide D2 Oligonuclectide D2 Oligonuclectide Dl Nuclectide sequenc Human tankyrasse2 e Novel human polynu Yeast AOD9604-asso EST R28562, fragme

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AAF58257

AAF58

5' end fragment of Oligonucleotide D1 Nucleic acid encod

AAF58238 AAC85314 AAV16949

AAF58238

Degenerate DNA seg Fragment P2-1 deri Fragment P2-9 deri

ALIGNMENTS

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aa:Xaa) aa:Xaa) aa:Xaa)

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(pos:1588. (pos:1594.

aa:Xaa)

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10 9 8 4 4 110

Result

2013, 2016, 2028, 2049, 2052,

aa:Xaa)

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Internal control

AAC85319 AAH48024 AAX80867

OM nucleic

Run on:

Sequence:

Searched:

Database

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PARP; poly ADP-ribose polymerase; metabolism; maize; transform; ss.
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   RESULT
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Fusion protein PAR
DNA encoding the p
DNA encoding the p
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hparp2 cDNA. Homo
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DNA encoding the p
DNA-binding domain
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Compugen Ltd.
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                                          GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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2949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                            The sequence is the maize poly ADP-ribose polymerase (PARP) gene. The sequence codes a PARP with 982 amino acids (AAY28464). PARP is required in the cell in most cases of DNA repair, recombination, rearrangement and transposition. PARP gene and antisense gene can be used to transform plant cells and alter the metabolic state of the transformed cell. This is useful in enhancing disease resistance in plants and methods of genetic transformation of plants. Plants transformed with either a sense or antisense PARP nucleotide sequence may be utilized to increase transformation frequency in plant cells. The enzyme also plays a role in cellular stress, so may be beneficial for prevention of plant disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                      useful in transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.6%; Score 2935.8; DB 20; Length 2949; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels 0;
                                                aa:Xaa)
aa:Xaa)
aa:Xaa)
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                                                                                                                                                                                                                                                                                                                    New maize poly ADP-ribose polymerase gene plants to alter their metabolic state
                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 30-35; 48pp; English.
                                                                                                                                                                                                                                      (PION-) PIONEER HI-BRED INT INC
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Matches 2949; Conserv
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Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
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cold; pathogen;
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                                ggaattcttagtcaagggctaagaattgcacctcctgaggcacctgttactggctatatg
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Page 103-108; 126pp; English.

The present sequence encodes the ZAP2 protein of Zee mays. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The ZAP2 polymucleotide sequences can be used for modulation of programmed cell death in evaluation of programmed cells and the method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous ZAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation contents that are resistant to fungion or nematodes; are male or female sterile, or have better seed-shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or complete plants)

T; 0 other; G; 823 C; 815 Sequence 3212 BP; 974 A; 600  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Best Local Similarity 98.33
Matches 2902; Conservative 61 121 181 381 201 261 241 321 301 361 441 421 501 481 561 541 621 501 681 199 741 q ò a ò Q ö g ŏ Q QQ g q οχ ογ ò ò Op Qγ g ò g ð 셤

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The present sequence encodes the ZAP1 protein of Zea mays. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The ZAP1 polymucleotide sequences can be used for modulation of programmed cell death in eukaryotic cells. The method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous ZAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation of plants that are resistant to fungil or nematodes; are male or female sterile, or have better seed-shatter properties. The methods are also used to improve growth of transformed plant cells (and derived calli or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
ZAP1; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter; ss.
                                                                                                                                                                                                                                                                            DNA encoding the poly(ADP-ribose) polymerase ZAP1 protein of Zea mays.
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/product= "ZAP1 protein"
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Matches 2869; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARP; DNA-binding domain; poly(ADP-ribose) polymerase; gene therapy;
tumour treatment; DNA repair; over-expression; ss.
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                                                                                                                                                                                                                                     ggattaggcaaaaccgtgccactggagtcagagtttgtgaagtggaagggatgatgtcgta
                                                                      gatgataaatatatgaaacttcactgtgacatcacccgctggctcacgatagtgaagat
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The present sequence encodes a poly(ADP-ribose) polymerase (PARP) contg. a DNA-binding domain (DBD). The DNA fragment from -29 to + 1127 (nucleotides 67-1220 of this sequence) encoding the DBD can be inserted into vectors which are used for gene therapy. Over-expression of the DBD inhibits the DNA repair function of PARP, so the vectors are useful for gene therapy or tumours, esp. in combination with conventional chemo-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 3793;
                                                                                                                                                                                                                                                                                                                                                                        Vectors contg. insert encoding DNA-binding domain of poly(ADP-ribose) polymerase - useful for gene therapy, esp. tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
7.6%; Score 24.0, 22.1,
Best Local Similarity 51.1%; Pred. No. 1.66-55;
Matches 693; Conservative 11; Mismatches 612; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3793 BP; 1049 A; 847 C; 1034 G; 863 T; 0 other;
              poly(ADP-ribose)_polymerase
                                                                  /*tag= b
/note= "encodes DNA-binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 224.6; DB 1
51.1%; Pred. No. 1.6e-55;
                                                                                                                                                                                                                                                      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                        Buerkle A, Kuepper J, Zur Hausen
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 1; 22pp; German.
                                "PARP"
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67..1220
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and/or radiotherapy
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This invention describes a novel vector (A), suitable for gene therapy, which contains a DNA insert (I) that encodes a practically complete to poly(deabnosine diphosphate-ribose) polymerase (PARP) which has antitumor activity. PARP is a nuclear DNA repair enzyme (activated by strand breakage), that allows recovery of proliferating cells from the toxic radiation), and protects cells against such damage or other causes of genomic instability. (A) are used for treatment of cancer and for cancer prevention in subjects at high risk (e.g. those with tunor-associated genetic defects). Tunor cells treated with (A) show an increased tendency to die when treated with radiation or chemotherapeutic agent, and in cells that survive this treatment they inhibit genomic instability, so should reduce the likelihood of further development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            both malignant cells and resistance to chemotherapy. This sequence encodes the human poly(ADP-ribose) polymerase described in the invention.
Gene therapy; poly(adenosine diphosphate-ribose) polymerase; treatment; PARP; antitumor; nuclear DNA repair; proliferating cell; DNA damage; protection; genomic instability; cancer; prevention; human; ds.
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                                                                                                                                                                                      /product= "poly(ADP-ribose) polymerase"
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                                                                                                                                                                                                                                                                                                                                                                                             (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New gene therapy vector expressing diphosphate-ribose)-polymerase for
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                                                                                 Homo sapiens
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                 2016 aaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccg
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The present invention provides the protein and coding sequence for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human tankyrase2 protein. This is found in two different versions, designated TANK2-LOGG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                            New tankyrase2 polypeptides, useful for treating conditions mediated poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1824 ggatgccattgagcagttcatgaaattatgaagaaaaaaccgggaacgcttggcactc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.5%; Score 219.8; DB 22; Length 3045; 50.9%; Pred. No. 3.8e-54; Live 11; Mismatches 615; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                    DL;
                                                                                                      SEQ ID NO: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3045 BP; 863 A; 710 C; 851 G; 621 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                    Goldman PS, McElligott
                                                                                                        tankyrase2 related coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 203-207; 242pp; English
                BP
                DNA; 3045
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                                                                                                                                                                                                                                                                             28-JUN-2000; 2000WO-US17827
                                                                           (first entry)
                                                                                                                                                      inflammatory disorder; ds
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P-PSDB; AAB66296.
              AAF63954 standard;
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                                                                                                                                                                                     Homo sapiens
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                                                                           05-APR-2001
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                                                              tgctatgatggaatttgaaawtaatatgtcagaaatgcctcttgggaagctaagcmaggr
                                                                                            2052 agccatggtggagtatgagatcgaccttcagaagatgcccttggggaagctgagcaaaag
                                                                                                                           2016 aaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccg
                                                                                                                                                            2112 gcagatccaggccgcatactccatcctcagtgaggtccagcaggcggt----gtctcag
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Human; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS;
inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia;
inflammation; ecebral vasospasm; rheumatoid arthritis; osteoarthritis;
W inflammation; ecebral vasospasm; rheumatoid arthritis; osteoarthritis;
W outy arthritis; spondylitis; Behcef's disease; sepsis; septic shock;
W endotoxic shock; gram negative sepsis; gram positive sepsis; trauma;
ttoxic shock syndrome; multiple organ injury syndrome; vasculitis;
W contrapage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy;
w connophilic granuloma; asthma; chronic bronchitis; allergic rhinitis;
w chronic obstructive pulmonary disease; slitosess; reperfusion injury;
w pulmonary sarcoidosis; pleurisy; alveolitis; pneumonia; myocardium;
bronchiectasis; pulmonary dyagen toxicity; keloid formation; brain;
scar tissue formation; atherosclerosis; systemic lupus erythematosus;
w cronic glomerulomephritis; untiple solerosis;
w chronic glomerulomephritis; inflammatory bowel disease;
w crohn's disease; ulcerative colitis; necrotizing entercolitis;
crohn's disease; ulcerative colitis; necrotizing entercolitis;
w psorlasis; urticaria; fever; myalgla; meninglits; encephalitis;
slogren's syndrome; alcoholic hepetitis; bacterial pneumonia;
w phypoolemic shock; Type I diabetes mellitus; hypersensitivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human poly(ADP-ribose) polymerase for treating inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leukocyte dyscrasia; thermal injury; cytokine-induced toxicity; expressed sequence tag; EST; RACE; PCR; amplify; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldman PS, McElligott DL;
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/product= "PARP1A/PARP2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 116-117; 129pp; English.
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                                                                                                        protein PARP1A/PARP2B cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymerase chain reaction; ds.
AAC85341 standard; cDNA; 3200
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                                                                       29-MAR-2001 (first entry)
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                                   AAC85341;
                                                                                                            Fusion
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This sequence encodes the fusion protein PARPIA/PARP2B. This protein contains amino acids 1-62 of hPARPI fused upstream of amino acids 230-583 of hPARP2. This sequence was amplified using the primer sequences given in AAC85311-40 and AAC85342-51. The fusion protein coding sequence was cloned in a baculovirus expression vector for the expression of the fusion protein. The protein of the invention, hPARP2, causes the covalent addition of polymers of ABP-ribose to protein targets. hPARP2 activity is induced in many instances of exidetive stress or during inflammation where there is direct damage to the DNA. hPARP2 may be used to identify

gaagtatctgctgaaactgaaattcaattttaaga 3031

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                                                                                                                                                                                                                                                                                                                                                                                                                                         1662 gtggggacgggttgggagtgagaaattggagggcaaaaactggaggagatgtcaaaaac 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1872 ctggggccgtgtgggtacggtgatcggtagcaacaaactggaacagatgccgtccaagga 1931
                                                                                                                                                                                                                                                                                                                           1602 ctactatgtactccagatcattgaacaggatgatgggtctgagtgctacgtatttcgtaa 1661
                                                                                                                                                                                                                                                                                                                                                                                  1812 ctactacaagctgcagcttctggaggacgacaaggaaaacaggtattggatattcaggtc 1871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2076 ctnatcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmatssytttttc
antagonists which may be used to treat a human having a disorder mediated by PARR2 activity, such as, inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders. hPARR2 and antibodies to it, can also be used to diagnose these conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2052 igaagaggcagigaagaagcigacagiaaaicciggcaccaaacgcgiiccagagicaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2016 aaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccg
                                                                                                                                                                                                                      DB 22; Length 3200;
                                                                                                                                                                                                                   Query Match
7.0%; Score 205.2; DB 22; Length
Best Local Similarity 49.9%; Pred. No. 8.2e-50;
Matches 675; Conservative 9; Mismatches 634; Indels
                                                                                                                                           Sequence 3200 BP; 923 A; 745 C; 870 G; 662 T; 0 other;
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Modulating cell death, growth and stress resistance in eukaryotes, specifically plants, used, e.g. to impart fungus or nematode resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAP; poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase; programmed cell death; apoptosis; growth rate; stress; cold; pathogen; pest; drought; heat; fungi; nematode; seed-shatter; ss.
                                                                                                                                                                                                                                                                                                3054 gaatccagatggttataccctcaactacaatgaatatattgtatataaccccaaccaggt 3113
                                                                                                                                                                                          2733 t---ccaagagggaagcattcgaccaagggattaggcaaaaccgtgccactggagtcaga 2789
                                                                                                                                                                                                                    2934 altgetteaaggtaaacatageaceaaggggetgggeaagatggeteeeagttetgeeea 2993
                                                                                                                                                                                                                                              2790 gittg-----tgaagitgaagggatgatgicgiagitccigcggcaagccggigccaic 2843
                                                                                                                                                                                                                                                                         2994 cttcgtcaccctgaatgggagtacagtgccattaggaccagcaagtgacacaggaattct 3053
                                                                                                    2814 ttccaagagtgccaattactgctttgcctctgcctaaagaatacaggactgctgctct 2873
                                                                                                                                          2673 ttotgaggttgctttaggagacatgtatgaactaaagaaagccacgtccatggacaaacc 2732
2694 gcatggttccaggatgagtaactgggtgggaatcttgagccatgggcttcgaattgccc 2753
                                   2613 aagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatgcttct
                                                                                                                                                          DNA encoding the poly(ADP-ribose) polymerase NAP protein.
                                                                                                                                                                                                                                                                                                                                                       2904 gaagatgcagttcttgctgaaggtgcgtttccat 2937
                                                                                                                                                                                                                                                                                                                                                                    3114 ccgtatgcggtaccttttaaaggttcagtttaat 3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "NAP protein'
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129..2042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ60617 standard; DNA; 2147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0118276.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 2000-182436/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY68835.
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Disclosure; Page 95-99; 126pp; English

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The present sequence encodes a NAP protein. This protein is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polynucleotide sequences can be used for modulation of programmed cell death in catavotic cells. The method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to viich PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant of stress (cold, chemical treatments, pathogens, pests, drought, heat, etc., or during transformation). Particular applications are generation of plants that are resistant to fungion nematedes; are male or female sterile; or have better seed-shatter properties. The methods are also contined to improve growth of transformed plant cells (and derived calli or
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Sequence 2147 BP; 704 A; 393 C; 496 G; 554 T; 0 other;

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1959 tatgatggaatttgaaawtaatatgtcagaaatgcctcttgggaagctaagcmaggraaa 2018
                                                                                                                                  1055 tatgatggaaataggatataacgctaacaattgccactcggcaagataagcaagtccac 1114
                                                                                                                                                                                2019 tattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccgctn 2078
                                                                                                                                                                                                                            1115 aatttcaaagggttatgaagtgctgaagagaatatcggaggtgattg-----accggta 1168
                                                                                                                                                                                                                                                                        2079 atcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmatssyttttcact 2138
                                                                                                                                                                                                                                                                                                                      1169 tgatagaacgaggcttgaggaactgagtggagagttctacacagtgatacctcatgattt 1228
                                                                                                                                                                                                                                                                                                                                                                                                           1229 tggttttaagaaaatgagtcagtttgttatagacactcctcaaaagttgaaacagaaat 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2199 gaaaatgottgaagototgcaggatattgaaattgottcaaaggatagttggottcgatag 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1289 tgaaatggttgaagcattaggtgaaattgaactcgcaacaaagttgttgtccgtcgaccc 1348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2259 cgacagt---gatgaatctcttgatgataaatatatgaaacttcactgtgacatcacccc 2315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1349 gggattgcaggatgatcctttatattatcactaccagcaacttaattgtgggtttgacgcc 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2316 gctggctcacgatagtgaagattacaagttaattgagcagtatctcctcaacacacatgc 2375
                                                     15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1409 agtaggaaatgattcagaggagttctctatggttgctaattacatggagaacactcatgc 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1469 aaagacgcattcgggatatacggttgagattgcccaactatttagagcttcgagagctgt 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2436 agaacttaataagtactcaagatataaaaataatctgcataacaagatgctattatggca 2495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2496 cggitcaaggitgacgaaiittgigggaaitctiagicaagggciaagaaiigcaccicc 2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1586 eggitcacgitcicaciaacigggeiggiatitiaicicaaggicigegaaiageiceiee 1645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1529 tgaagctgatcgattccaacagttttcaagtt---cgaagaacaggatgctactctggca 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caagagegeacaatactgttatgtggataggaataateetgtaggtttgatgettettte 2675
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                                                                                                                                                                                                                                                                                                                                                                 2139 cttatcccttctattcatcctcatattatacgggatgaggatgatttcatattcaaaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2376 tcctactcacaaggactggtcgctggaactggaggaagttttttcacttgatcgagatgg
  6.9%; Score 204.4; DB 21; Length 2147; 52.3%; Pred. No. 1.1e-49; tive 11; Mismatches 449; Indels 15;
                                           Matches 521; Conservative
                        Similarity
Query Match
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is a poly(ADP-ribose) polymerase (PARP) protein (also known as poly(ADP-ribose) transferase). The PARP enzyme is involved in programmed cell death or apoptosis, and is a nuclear enzyme. The NAP polynucleotide sequences can be used for modulation of programmed cell death in elekaryotic cells. The method is used, specifically in plants, to induce, or protect against, programmed cell death, depending on the extent to which PARP activity is reduced. Reducing expression of endogenous NAP class PARP only is also used to modulate programmed cell death, to increase growth rate and to produce plant cells that are more tolerant

The present sequence encodes the NAP protein of Zea mays. This protein

Example 1; Page 89-92; 126pp; English.

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tgtgaagtggaaggatgatgtcgtagttccctgcggcaagccggtgccatcatcaattag 2852
                                                                                                                                                                1946 caaggggatgttgttgtacaacgaatatatagtctacaatgtggaacaaatcaagatgcg 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specifically plants, used, e.g. to impart fungus or nematode resistance
                                                tccaagagggaagcattcgaccaagggattaggcaaaaccgtgccactggagtcagagtt 2792
                                                                       accccggggaaagctaagcacaaaaggtgtggggaaacagcaccaaacccatcagaggc 1885
                                                                                                                    tcaaacactagaagacggtgttgttgttccacttggcaaaccagtggaacgttcatgctc 1945
                                                                                                                                                                                                                                                                                                                                                                                programmed cell death; apoptosis; growth rate; stress; cold; pathogen;
pest; drought; heat; fungi; nematode; seed-shatter; ss.
                                                                                                                                                                                                                                                                                                                                                                      poly(ADP-ribose) polymerase; PARP; poly(ADP-ribose) transferase;
                                                                                                                                                                                                                                                                                                                                             DNA encoding the poly(ADP-ribose) polymerase NAP protein of Zea mays.
                                                                                                                                         2853 gagctctgaactcatgtacaatgagtacatcgtctacaaccatcccaggtgaagatgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating cell death, growth and stress resistance in eukaryotes,
                                                                                                                                                                                       2913 gttcttgctgaaggtgcgtttccatcacaagaggta 2948
                                                                                                                                                                                                             2006 ttatgtgatccaagtcaaattcaactacaagcacta 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "NAP protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Block M;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                        AAZ60616 standard; DNA; 2295 BP
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                                                                                                                                                                                                                                                                                                                       16-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..2068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kushnir S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-182436/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-1999;
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                                                                                                                                                                                                                                                                                                AAZ60616;
                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays.
                                               2733
                                                                      1826
                                                                                                                   1886
                                                                                              2793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1550 ggtgaaacagagcgatttcaaaaatttgctagtacaaga---aataggatgctttgtgg 1606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1490 ggaaaaacacactctggttatacggtggacatagtgcaaatatttaaggtttcaaggcat 1549
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                                                                                                                                                                                                                                       6.8%; Score 200.2; DB 21; Length 2295; 51.8%; Pred. No. 2e-48;
                                                                                                                                                                                                                                                                                         Matches 546; Conservative 12; Mismatches 482; Indels
                                                                                                                                                                      Sequence 2295 BP; 668 A; 447 C; 597 G; 583 T; 0 other;
                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                      complete plants)
                                                                                                                                                                                                                                                         Query Match
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1847 ctgcccaaaggaaaattaagatccaagggagttggtcaaacagcacctaacatggtcgag 1906

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This sequence represents cDNA encoding a novel human poly(ADP-ribose)
synthetase, sbhPARS2. The invention also relates to fragments,
synthetase, sbhPARS2. The invention also relates to fragments,
constraints and sequences with at least 95% identify to the sbhPARS2
comprising an explexes acid sequence; the recombinant expression
comprising an antibody specific for sbhPARS2 sbhPARS2 sproteins
compounds which inhibit or stimulate its activity or expression level.
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compounds which inhibit or stimulate its activity or expression level.
compounds defined and antagonists of sbhPARS2 are useful for treating human
classase including ischaemia and ischaemic tissue injury (e.g., cerebral
autoimmune disease (e.g., diabetes, multiple sclerosis) and
autoimmune disease (e.g., Parkinson's disease and Alzheimer's
chaemas in sbhPARS2 nucleic acids are useful as diagnostic reagents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic assays and for screening modulators used for preventing and treating inflammation, autoimmune disease and Alzheimers disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; poly(ADP-ribose) synthetase; sbhPARS2; vaccine; drug screening; ischaemic disorder; cerebral ischaemia; cardiac ischaemia; myocardial infarction; stroke; inflammation; autoimmune disease; diabetes; multiple sclerosis; neurodegenerative disease; Parkinson's disease; Alzheimer's disease; chromosome localisation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Human poly(ADP-ribose) synthetase sbhPARS2"
                     2851 aggagctctgaactcatgtacaatgagtacatcgtctacaacacatcccaggtgaagatg 2910
                                                                                                                       1967 aaaaggggtggcttgctttataatgagtacatagtgtacaacgtagaccagataagaatg 2026
2791 tttgtgaagtggagggatgatgtcgtagttccctgcggcaagccggtgccatcatcaatt 2850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human polypeptide of the polyADPribose synthetase family for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Human poly(ADP-ribose) synthetase sbhPARS2 cDNA.
                                                                                                                                                                     2911 cagttcttgctgaaggtgcgtttccatcacaagag 2945
                                                                                                                                                                                                              2027 cggtatgtcttacatgttaacttcaatttcaagag 2061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 21; 30pp; English.
                                                                                                                                                                                                                                                                                                                     AAF59996 standard; cDNA; 1566 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2001 (first entry)
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detecting mutations in the associated gene; as hybridisation probes to isolate full-length subpARS2 CDNAs and sbhPARS2 genomic clones; and for chromosome localisation studies. The sbhPARS2 protein is also useful as an immunogen to produce antibodies for therapeutic use. sbhPARS2 proteins, nucleotides and antibodies are also useful in screening methods for detecting the effect of added compounds on the production of mRNA and protein in cells.
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Sequence 1566 BP; 490 A; 328 C; 381 G; 367 T; 0 other;

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                                                                                1833 tgatgitgattatggtgitaagaaagcaccaaaacggaaagatatcagtgaaatgaaag 1892
                                                                                                                                                                 1893 ttotottgotcotcaattgotagaactcatgaagatgottttcaatgtggagacatatag 1952
                                                                                                                                                                                                                                                      1953 agctgctatgatggaatttgaaawtaatatgtcagaaatgcctcttgggaagctaagcma 2012
                                                                                                                                                                                                                                                                                                                                       2013 ggraaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggaca 2072
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      DB 22; Length 1566;
                        Pred. No. 4.8e-46;
9; Mismatches 508; Indels
    6.5%; Score 191.8; 51.0%; Pred. No. 4.8
                                   Matches 570; Conservative
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Whuman; poly(ADP-ribose) polymerase; hPARP2; oxidative stress; ARDS;
Inflammation; ischaemic stroke; hemorrhagic shock; myocardial ischemia;
Inflammation; cerebral vasosepasm; rheumatoid arthritis; oxecarthritis;
W gouty arthritis; spondylitis; Behcet's disease; sepsis; septic shock;
w endotoxic shock; gram negative sepsis; gram positive sepsis; trauma;
W toxic shock syndrome; multiple organ injury syndrome; vasculitis;
W hemorrhage; conjunctivitis; uveitis; thyroid-associated ophthalmopathy;
w obsinophilic granuloma; asthma; chronic bronchitis; allergic rhinitis;
W pulmonary sarcoidosis; pleurisy; alveolitis; pneumonia; myocardium;
W pronchiectasis; pulmonary oxygen toxicity; keloid formation; brain;
Scar tissue formation; atherosclerosis; systemic lupus erythematosus;
W autoimmune thyroiditis; uniltiple solerosis; Reynaud's syndrome;
W graft versus host disease; allograft rejection; cystic fibrosis;
W crohn's disease; allograft rejection; cystic fibrosis;
W crohn's disease; ulografty collitis; necrotizing entercollitis;
                                                                            1332 aggattgetteaaggtaaacatageaceaaggggetgggeaagatggeteecagttetge 1391
                                                                                                                    2787 agagtttg----tgaagtggagggatgatgtcgtagttccctgcggcaagccggtgcc 2840
1272 cttatcagaggtagctctaggtcagtgtaatgaactactagaggccaatcctaaggccga 1331
                                                                                                                                                          1392 ccacttcgtcaccctgaatgggagtacagtgccattaggaccagcaagtgacacaggaat 1451
                                                                                                                                                                                                                          inflammatory dermatosis; contact dermatitis; atopic dermatitis; sportasis; urticaria; fever; myajqia; meningitis; encephalitis; Sjogren's syndrome; alcoholic hepatitis; bacterial pneumonia; hypovolemic shock; Type I diabetes mellitus; hypersensitivity; leukocyte dyscrasia; thermal injury; cytokine-induced toxicity; ds.
                                        ---acctccaagagggaagcattcgaccaagggattaggcaaaaccgtgccactggagtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "hPARP2"
                                                                                                                                                                                                                                                                                                                                                                                                                         AAC85303 standard; cDNA; 1814 BP
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us-09-236-995d-1.rng

neurological, cardiovascular, or neoplastic tissue growth disorders, such as, arthritis, encephalitis, myocardial ischemia, and leukocyte metastasis New human poly(ADP-ribose) polymerase for treating inflammatory,

Claim 1; Page 91-93; 129pp; English.

to the DNA. hPARP2 may be used to identify antagonists which may be used to treat a human having a disorder mediated by PARP2 activity, such as, inflammatory, neurological, cardiovascular, or neoplastic tissue growth disorders, e.g. ischemic stroke, myocardial ischemia or infarction, transplantation, cerebral vasospasm; rheumatoid, osteo- or gouty arbock, gram negative or positive sepsis, toxic shock syndrome; multiple organ injury syndrome secondary to septicemia, trauma, or hemorrhage; allergic or vernal conjunctivitis, uveits, thyroid-associated ophthalmopathy; eosinophilic granuloma; asthma, chronic bronchitis, allergic rhinitis, ARDS, chronic obstructive pulmonary disease, silicosis, pulmonary sarcoidosis, pleurisy, alveolitis, vasculitis, pneumonia, pronchiectasis, pulmonary oxygen toxicity; reperfusion injury of the myocardium, brain or extremilies; cystic fibrosis; keloid formation, scar tissue formation; atherosclerosis; systemic lupus cryndrome; graft versus host disease, allograft rejection; chronic glomerulonephritis; inflammatory bowel disease, Crohn's disease, contain, and manalory dermaloses. antigen-antibody complex mediated diseases; hypovolemic shock; Type 1 diabetes mellitus; acute and delayed hypersensitivity; disease states due to leukozyte dyscrasia and metastasis; thermal injury; granulocyte transfusion associated syndromes; and cytokine-induced toxicity. hPARP2 and antibodies to it, can also be used to diagnose these myalgias contact or atopic dermatitis, psoriasis, urticaria, fever and myalgiass due to infection; meningitis, encephalitis, and brain and spinal cord injury due to minor trauma; Sjogren's syndrome; diseases involving leukocyte diapedesis; alcoholic hepatitis; bacterial pneumonia; This sequence encodes human poly(ADP-ribose) polymerase (hPARP2). This protein causes the covalent addition of polymers of ADP-ribose to protein targets. hPARP2 activity is induced in many instances of oxidative stress or during inflammation where there is direct damage. 

Sequence 1814 BP; 558 A; 389 C; 462 G; 405 T; 0 other;

Š. tgatgttgattatggtgttaagaaagcaccaaaacggaaagatatcagtgaaatgaaaag 1892 1893 ttetettgeteeteaattgetagaaeteatgaagatgetttteaatgtggagacatatag 1952 2012 2013 ggraaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggaca 2072 2133 ttcactcttatcccttctattcatcctcatattatacgggatgaggatgattcatattc 2192 tecgeatgaetttggaetecgtaetectecaetaatecggaeacagaaggaaetgteaga 1048 Gaps 698 tcaggatgaagaggaaacaaagaagaaggaatctettaaatetecettgaagecagagte 1953 agctgctatgatggaatttgaaawtaatatgtcagaaatgcctcttgggaagctaagcma 818 agaaatgatgatgaaatgaagtataataccaagaaagccccacttgggaagctgacagt 2073 ccgctnatcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmatssyttt ccagcatggacgagctctcatggaagcatgcaatgaattcta-----caccaggat Length 1814; 30; 9; Mismatches 508; Indels Score 191.8; DB 22; Pred. No. 5.3e-46; 1 6.5%; Similarity 51.0%; 570; Conservative Query Match Best Local S 686 Matches 1833 938 οy g Db δ g Qγ q δλ 셤

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1460 gtcttccaagagtgccaattactgctttgcctctcgcctaaagaatacaggactgctgct 1519
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2193 aaaggogaaaatgottgaagototgoaggatattgaaattgottoaaagatagttggott 2252
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                1169 gegececettgaceatgaaagttaegagtteaaagtgattteeeagtaeetaeaatetae
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                                                                    2253 cgatagcgacagtgatgaatctc---ttgatgataaatatatgaaacttcactgtgacat
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/product= "PARP2"
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This invention describes novel human and murine poly(ADP-ribose)
polymerase (PARP) homologues, which are characterised by an amino acid
sequence with a functional NAD<sup>+</sup>-binding site and no zinc finger
sequences with a functional NAD<sup>+</sup>-binding site and no zinc finger
sequences. PARP homologues and antibodies are useful for analytic
detection of PARP homologues and for identifying PARP effectors or
binding partners, as well as for determining their effectiveness.
PARP-binding partners are useful for the diagnosis or therapy of a
disease condition, which is the result of a PARP protein, especially an
classase condition, which may comprise tissue damage from cell death
following necrosis or apoptosis. The disease condition may be chosen
from a neurodegenerative illness, or sepsis or ischemic tissue damage,
in particular neurotoxic disturbances, etc. This sequence encodes the
human PARP2 protein used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                           Novel genes and proteins, antibodies and binding partners useful in diagnosis and therapy of energy deficiency associated disease conditions -
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                                                                                                                                                                                                                                    Lubisch W,
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                                                                                                                                                                                                                              Otterbach B,
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7a; Page 49-52; 96pp; German,
                                                                                                                                                                                                                              Kock M, Hoeger T, Kroeger B,
                                                                                                                                  98DE-1025213.
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                                                                                                                                                                                                                                                                    WPI; 2000-087218/07.
P-PSDB; AAY51174.
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                   W09964572-A2
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  6.5%; Score 191.8; DB 21; Length 1843; 51.0%; Pred. No. 5.3e-46;
                                         9; Mismatches 508; Indels
                 Local Similarity 51.0 les 570; Conservative
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Human brain poly-ADP-ribose-polymerase cDNA. AAC82090 standard; cDNA; 1843 BP (first entry) 02-MAR-2001 AAC82090; RESULT 13 AAC82090

cerebroprofective, antiparkinsonian, nephrotropic, cardiant, vasotropic, anticonvulsant; cytostatic; antibacterial; immunosuppressive; treatment, antinflammatory; antirheumatic; antiarthritic; antidiabetic; epilepsy; 2H-phthalazin-1-one derivative; neurodegenerative disease; tumor; neuronal damage; Alzheimer's disease, Huntington's disease; metastasis; Parkinson's disease; ischemic damage; microinfarction; sepsis; Human; poly ADP-ribose polymerase; PARP; neuroprotective; nootropic; diabetes mellitus; ss.

Homo sapiens

DE19921567-A1 

16-NOV-2000.

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Parkinson's disease), treating or preventing ischemic damage
CC (specifically renal damage after renal ischemia or during and after
CC (specifically renal damage after renal ischemia), treating
CC kidney transplantation or heart damage after cardiac ischemia), treating
CC epilepsy, specifically generalized epileptic attacks (e.g. petit mal and
CC conic-clonic attacks) or partial epileptic attacks (e.g. temporal lope
CC donic-clonic attacks), treating malcrohifarction (e.g. during and
CC after heart valve replacement, aneurysm resectioning and heart
CC after heart valve replacement, aneurysm resectioning and heart
CC arteries (e.g. after PCTA or by pass operations) or peripheral arteries
CC arteries; (e.g. after PCTA or by pass operations) or peripheral arteries
CC after its mechanical or drug-induced lysis and treating tumors and
CC after metastasis, sepsis and septic shock, inflammatory and rheumatic
CC their metastasis, sepsis and septic shock, inflammatory and rheumatic
CC their metastasis, sepsis and septic shock, inflammatory and rheumatic
CC their matastasis, sepsis and septic shock, inflammatory and rheumatic
CC their matastasis, sepsis and septic shock, inflammatory and rheumatic
CC their matastasis, sepsis and septic shock, inflammatory and rheumatic
CC their matastasis, sepsis and septic shock, inflammatory and the multiply the particular (I) have very strong PARP2 inhibitory activity (e.g. with K_i values of 1-20 nM) and high selectivity for PARP2 relative to
CC ARRP1 (generally by a factor of more than 5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derivatives (I) which are used for the treatment or prophylaxis of diseases associated with elevated poly (ADP-ribose)-polymerase (PARP; EC 2.4.2.30) activity. The products of the invention have moortopic, neuroprotective, cerebroprotective, antiparkinsonian, nephrotropic, anticonvulsant, cytostatic, antibacterial, immunosuppressive, antinfammatory, antirheumatic, antiarthritic, antidabhetic. (I) are specially used for treating or preventing neurodemerative disease or neuronal damage (specifically associated with ischemia, trauma or massive bleeding, especially apoplexy or partires, antiment of antidation or disease or neuronal damage (specifically associated beting location).
                                                                                                                                                                                                                                                                                                  Drugs for inhibiting PARP or especially homologous enzymes comprising 4-substituted phthalazinone derivatives, useful e.g. for treating neurodegenerative disease, ischemic damage, tumors or diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel 4-substituted 2H-phthalazin-1-one
                                                                                                                                                               Lubisch W, Sadowski J, Kock M, Hoeger T;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example A; Page 9-12; 14pp; German.
99DE-1021567
                                                        99DE-1021567
                                                                                                                                                                                                                                    WPI; 2001-032983/05.
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                                                                                                                      (BADI ) BASF AG.
      11-MAY-1999;
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Sequence 1843 BP; 599 A; 377 C; 447 G; 420 T; 0 other;

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                                                                                                                           1893 tectettgetecteaattgetagaacteatgaagatgettteaatgtggagaeatatag 1952
                                                                                                                                                                                                                                                                                      779 ggcacaaatcaaggcaggttaccagtctcttaagaagattgaggattgtattcggggctgg 838
                                                                                                                                                  719 agaaatgatgatggaaatgaagtataataccaagaaagccccacttgggaagctgacagt 778
                                                                                             599 tcaggatgaagagaaacaaagaaagaaggaatctcttaaatctcccttgaagccagagtc 658
6.5%; Score 191.8; DB 22; Length 1843; 51.0%; Pred. No. 5.3e-46; tive 9; Mismatches 508; Indels 30;
                                          Matches 570; Conservative
                           Best Local Similarity
             Query Match
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Human: open reading frame, ORFX; detection; cytostatic; hepatotropic;
vulnerary: antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant;
immunostimulant; thrombolytic; coaqulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2841 atcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacacatccca 2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1601 totgaatocagatggttatacoctcaactacaatgaatatattgtatataaococaacca 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2787 agagtttg-----tgaagtggagggatgatgtcgtagttccctgcggcaagccggtgcc 2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1541 ccacttogtcaccctgaatgggagtacagtgccattaggaccagcaagtgacacaggaat 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2730 ---acctccaagaggaagcattcgaccaagggattaggcaaacgtgccactggagtc 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1481 aggattgettcaaggtaaacatagcaccaaggggetgggcaagatggeteccagttetge 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1301 cccacctgaagetcccatcacaggttacatgtttgggaaaggaatctactttgctgacat 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2610 agtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatgct 2669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1361 gtottocaagagtgocaattactgotttgoctotogoctaaagaatacaggactgotgot 1420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2550 acctcctgaggcacctgttactggctatatgttcggcaaaggcctctactttgcagatct 2609
                                                                                                                                                                                                                                                                                                                                                                                                                             2430 agatggagaacttaataagtactcaagatataaaaataatctgcataacaagatgctatt 2489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2490 atggcacggttcaaggttgacgaattttgtggggaattcttagtcaagggctaagaattgc 2549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1241 atggcatggttccaggatgagtaactgggtgggaatcttgagccatgggcttcgaattgc 1300
                                                                                                                                                                                                                                                                                                                                                   2370 acatgotoctactcacaaagactggtcgctggaactggaggaagtttttcacttgatcg 2429
                                                                                                                                                                                                                                                                                                                                                                                          1130 ccatgotoccacacacacagogactataccatgaccttgctggattgtttgaagtggagaa 1189
                                                                                                                                                                                                                                                                                                           1070 gcgccccttgaccatgaaagttacgagttcaaagtgatttcccagtacctacaatctac 1129
                                                                                                                                                                                                                                                                        2310 cacccogotggctcacgatagtgaagattacaagttaattgagcagtatctcctcaacac 2369
                                                                                                                2193 aaaggcgaaaatgcttgaagctctgcaggatattgaaattgcttcaaagatagttggctt 2252
                                                                                                                                                       2253 cgatagcgacagtgatgaatctc---ttgatgataaatatatgaaacttcactgtgacat 2309
                                                                                                                                                                                                                  2133 ttcactcttatcccttctattcatcctcatattatacgggatgaggatgatttcatattc 2192
                                                                          890 tecgcatgaetttggaetecgtaetectecaetaatecggaeacagaaggaaetgteaga 949
839 ccagcatggacgagctctcatggaagcatgcaatgaattcta-----caccaggat 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX ORF2673 polynucleotide sequence SEQ ID NO:5345.
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antiviral, antibacterial, antifungal, antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; cardiovascular disease; diabetes mellitus; graft vs host disease; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; bone damage; cartilage damage; antiinflammatory disease; cartilage damage; antiinflammatory disease; coagulation;
hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; contraceptive; ss.
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Homo sapiens.

WO200058473-A2.

05-0CT-2000

31-MAR-2000; 2000WO-US08621.

02-APR-1999; 99US-0127636. 05-APR-1999; 99US-0127728. 30-MAR-2000; 2000US-0540763. 99US-0127607 31-MAR-1999;

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2000-602362/57.

P-PSDB; AAB42909.

Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -

Claim 5; Page 4521-4522; 5507pp; English.

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORPX open reading frames 1 to 3161. The ORPX sequences have activities such as: cytostatic; hepatotropic; vulnerary; catiporatatic; antiporatanic antiarthritic; immunosuppressant; immunosuppressant; immunosuppressant; immunostimulant: cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressant; cantinflammatory; antiboreticial antiviral; antifungal; antithumatic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; cantidiabetic; hypotensive; dermatological; antithusical; antibuagical; antithusical; antibuagical; antithusical; antibuagical; antithusical; antibuagical; antibuag coagulation; to inhibit thrombosis; and as a contraceptive. 

Sequence 1912 BP; 620 A; 390 C; 467 G; 433 T; 2 other;

1833 tgatgttgattatggtgttaagaaagcaccaaaacggaaagatatcagtgaaatgaaag 1892 1893 ttctcttgctcctcaattgctagaactcatgaagatgcttttcaatgtggagacatatag 1952 6.5%; Score 191.8; DB 21; Length 1912; 51.0%; Pred. No. 5.5e-46; ative 9; Mismatches 508; Indels 30; Gaps 663 tcaggatgaagagaaacaaagaagaagaatetettaaateteeettgaagecagagte 722 723 acagciagatettcgggtacaggagttaataaagttgatctgtaatgttcaggccatgga 782 Conservative Similarity Matches 570; Query Match Best Local ò g g

1953 agctgctatgatggaatttgaaawtaatatgtcagaaatgcctcttgggaagctaagcma 2012 2013 ggraaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggaca 2072 2073 ccgctnatcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmatssyttt 2132 2133 ttcactcttatcccttctattcatcctcatattatacgggatgaggatgatttcatattc 2192 954 tecgeatgaetttggaetecgtaetectecaetaateeggaeacagaaggaactgteaga 1013 2193 aaaggogaaaatgottgaagototgoaggatattgaaattgottoaaagatagttggott 2252 1014 aaaaatacaattactagaaggetttgggagacattgaaattgctattaagctggtgaaaac 1073 783 agaaatgatgatggaaatgaagtataataccaagaaagccccacttgggaagctgacagt 842 903 ccagcatggacgagctctcatggaagcatgcaatgaattcta-----caccaggat 953 2253 cgatagcgacagtgatgaatctc---ttgatgataaatatatgaaacttcactgtgacat 2309 1074 agagctacaaaggcccagaacaccattggaccaacactatagaacctacattgtgcctt 1133 2310 cacccgctggctcacgatagtgaagattacaagttaattgagcagtatctcctcaacac 2369 | 1134 gcgccccttgaccatgaaagttacgagttcaaagtgatttcccagtacctacaatctac | 1193 2370 acatgotoctactcacaaggactggtcgctggaactggaaggttttttcacttgatcg 2429 1194 ccatgotoccacacacagogactataccatgacottgotggatttgtttgaagtggagaa 1253 2430 agaiggagaacttaataagtactcaagatataaaaataatctgcataacaagatgctatt 2489 2490 atggcacggttcaaggttgacgaattttgtgggaattcttagtcaagggctaagaattgc 2549 1254 ggatgg-----tgagaaagaagcettcagagaggacettcataacaggatgetet 1304 2550 acetectgaggcacetgttactggetatatgtteggcaaaggeetetaetttgeagatet 2609 2610 agtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatgct 2669 1425 gtcttccaagagtgccaattactgctttgcctctcgcctaaagaatacaggactgctgct 1484 2670 tetttetgaggttgetttaggagacatgtatgaactaaagaaagccacgtecatggacaa 2729 2730 ---acctccaagaggaagcattcgaccaagggattaggcaaaaccgtgccactggagtc 2786 1485 ctiatcagaggtagctctaggtcagtgtaatgaactactagaggccaatcctaaggccga 1544 2787 agagtttg-----tgaagtggagggatgatgtcgtagttccctgcggcaagccggtgcc 2840 1605 ccacttcgtcaccctgaatgggagtacagtgccattaggaccagcaagtgacacaggaat 1664 2841 atcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacacatccca 2900 2901 ggtgaagatgcagttcttgctgaaggtgcgtttccat 2937 1725 ggtccgtatgcggtaccttttaaaggttcagtttaat 1761 g g ò g ò QQ Q ò Op οy QQ qq δ δ qq δλ g δy g δ g g Óγ q ò q

RESULT 15

AAH14941 standard; cDNA; 1980 BP.

the present invention describes pramer sets for synthesisting 300.2

full-length connact connected in the specification. Where a primer set

comprises: (a) an oliqo-for primer and an oligonucleotide complementary

cc to the complementary strand of a polynucleotide which comprises one of

the 560 nucleotide sequences defined in the specification, where the

oligonucleotide comprising a sequence complementary to the

cc an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

complementary strand of a polynucleotide which complementary to a

complementary strand of a polynucleotide which complementary to a

complementary strand of a polynucleotide where the

complementary strand of a polynucleotide where the

cc plynucleotide which comprises a 1'-end sequence complementary to a

coligonucleotide comprises at least 15 nucleotides and the combination of

the 5'-end sequence/1'-end sequence is selected from those defined in

the specification. The primers are useful for synthesisising polynucleotides,

cc particularly full-length cDNAs. The primers are also useful for the

cc particularly full-length cDNAs. The primers are also useful for the

cc cDNAS aeasily without any specialised methods. AAH03166 to AAH13628 and

cc AAH13633 to AAH18412 represent human cDNA sequences; AAB92446 to

ABB95893 represent human amino acid sequences; and AAH13629 to AAH13632

crepresent oligonucleotides, all of which are used in the exemplification Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the The present invention describes primer sets for synthesising 5602 oca r, isogai T, Nishikawa T, Hayashi K, Saito K, Y. Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T; Sequence 1980 BP; 618 A; 413 C; 486 G; 463 T; 0 other; Claim 8; SEQ ID 12843; 2537pp + CD ROM; English. Human cDNA sequence SEQ ID NO:12843. 27-AUG-1999; 99JP-0300253. 11-JAN-2000; 2000JP-0118776. 02-MAY-2000; 2000JP-0183767. 09-JUN-2000; 2000JP-0241899. 28-JUL-2000; 2000EP-0116126 26-JUN-2001 (first entry) of the present invention. (HELI-) HELIX RES INST WPI; 2001-318749/34. full-length cDNAs -Homo sapiens EP1074617-A2 29-JUL-1999; 07-FEB-2001 AAH14941; 

4 Gaps 6 3%; Score 185.4; DB 22; Length 1980; 52.2%; Pred. No. 4.4e-44; Indels 422; 9; Mismatches Best Local Similarity 52.2 Matches 496; Conservative Query Match

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1893 ttctcttgctcctcaattgctagaactcatgaagatgcttttcaatgtggagacatatag 1952

2670 tetttetgaggttgetttaggagacatgtatgaactaaagaaagecaegteeatggacaa 2729 2550 acctcctgaggcacctgttactggctatatgttcggcaaaggcctctactttgcagatct 2609 2610 agtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatgct 2669 1403 gtcttccaagagtgccaattactgctttgcctctcgcctaaagcatacaggactgctgct 1462 2430 agatggagaacttaataagtactcaagatataaaaataatctgcataacaagatgctatt 2489 1232 ggatggtg-----agaaagaagccttcagagaggaccttcataacaggatgcttct 1282 2490 atygcacggttcaaggttgacgaattttgtgggaattcttagtcaayggctaagaattgc 2549 2370 acatgotoctactcaccaaggactggtcgctggaactggaggaagtttttcacttgatcg 2429 1172 ccatgotoccacacacagogactataccatgacottgotggatttgtttgaagtggagaa 1231 2310 caccccgctggctcacgatagtgaagattacaagttaattgagcagtatctcctcaacac 2369 2073 ccgctnatcaagcactggcttgttrgagaaagctnaattgttgytgsgagcmatssyttt 2132 2133 tteactettateeettetatteateeteatattataegggatgaggatgattteatate 2192 2193 aaaggcgaaaatgcttgaagctctgcaggatattgaaattgcttcaaagatagttggctt 2252 2253 cgatagcgacagtgatgaatctc---ttgatgataaatatatgaaacttcactgtgacat 2309 2013 ggraaatattgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggaca 2072 1953 agctgctatgatggaatttgaaawtaatatgtcagaaatgcctcttgggaagctaagcma 2012 || |||||||||| || :|||||| 821 ggcacaaatcaaggcaggttaccagtctcttaagaagattgaggattgtattcgggctgg 880 932 teegeatgaettiggaeteegtaeteeteeaetaateeggaeaeaggaaetgteaga 991 881 ccagcatggacgagctctcatggaagcatgcaatgaattcta-----caccaggat 931 701 acagctagatcttcgggtacaggagttaataaagctgatctgtaatgttcaggccatgga 760 761 agaaatgatgatggaaatgaagtataataccaagaaagccccacttgggaagctgacagt 820 aggattgcttcaaggtaaacatagcaccaaggggctgggcaagatggctcc 1573 2730 ---acctccaagagggaagcattcgaccaagggattaggcaaaaccgtgcc 2777 Dβ Qγ Dp qq qq QΥ qq ά ōλ Qγ δλ Q Qγ Qλ qq δλ g δ qq Ω

Yamamoto

Search completed: March 7, 2002, 18:16:17 Job time: 13267 sec

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US-08-328-111-216

US-08-328-114-216

US-08-331-398A-22

US-08-331-398A-22

US-08-331-398A-60

US-08-331-397B-60

US-08-331-397B-60

US-08-32-3

US-08-32-3

US-08-32-3

US-08-59-804A-59

US-08-50-80-3

US-08-50-90-3

US-08-50-90-3

US-08-60-90-3

US-08-60-90-3

US-08-60-90-3

US-08-60-90-3

US-08-60-90-3

US-08-181-271A-21

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US-08-444-803-21
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METHOD OR DETECTING A PREDISPOSITION TO CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,618
FILING DATE: 19930406
CLASSIFICATION A 435
PROR APPLICATION DATA:
APPLICATION NUMBER: US/07/257,696
FILING DATE: 14-OCT-1988
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAMIET I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Score 219.8; DB 1;
50.9%; Pred. No. 2.1e-55;
ive 11; Mismatches 615;
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CORRESPONDENCE ADDRESS:
STREET: 1225 Connecticut Suite 300
US-08-456-265A-21
US-08-455-416-21
US-08-454-876-21
US-08-454-876-21
US-08-456-262-21
US-08-456-262-21
US-08-455-736-21
US-08-455-736-21
US-08-455-736-21
US-08-335-469-1
US-08-477-504A-1
US-08-486-756A-1
US-08-487-862B-1
US-08-487-862B-1
US-08-487-7304A-1
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REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0654.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)466-0800
TELEFAX: (202)833-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: ZUDJU
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-044-618-5; Sequence 5, Application US/08044618; Patent No. 5449605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SMULSON, MARK
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: CANCER
TITLE OF INVENTION: POLYMEI
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3747 base pairs
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       NUCLEIC ACID
EDNESS: both
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OPERATING SYSTEM:
SOFTWARE: PatentI
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CITY: Washington
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                                                                      1662 gtggggacgggttgggagtgagaaaattggagggcaaaaactggaggagatgtcaaaaac 1721
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METHOD OR DETECTING A PREDISPOSITION TO CANCER BY THE USED OF RESTRICTION FRAGMENT LENGTH POLYMORPHISM OF THE GENE FOR THE HUMAN POLY (ADP-RIBOSE)
2950 GTTGGGAGAAGTTGCCCTTGGAAACATGTATGAACTGAAGCACGCTTCACATATCAGCAG 3009
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                                                                   acctccaagagggaagcattcgaccaagggattaggcaaaaccgtgccactggagtcaga
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CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/044,618
FILING DATE: 19930406
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Pred. No. 2.1e-37;
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                                                                                                                                                                                                                                                                                                                                                             3187 GAAGTATCTGCTGAAACTGAAATTCAATTTTAAGA 3221
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NAME: FOX SAMUEL L

REGISTRATION NUMBER: 30,353

REGISTRATION NUMBER: 0654.0490001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/257,696
FILING DATE: 14-OCT-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08044618
Patent No. 5449605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202)466-0800
TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: CANG
TITLE OF INVENTION: POLY
TITLE OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kes
STREET: 1225 Connection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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PRIOR APPLICATION DATA:
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APPLICANT: SMULSON,
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US-08-044-618-7
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RESULT
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                                         3364 CAGAGATICTGAAGAAGCTGAGATCATCAGGAAGTATGTTAAGAACACTCATGCAACCAA 3423
                                                                                                                     3424 CCACACACGATG--CATATGACTTGGAAGTCATTGATAGCTTTAAGATAGAGTGTGAAGA 3481
                                                                                                                                                              2439 acttaataagtactcaagatataaaaatatetgcataacaagatgctattatggcacgg 2498
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2322 tcacgatagtgaagattacaagttaattgagcagtatctcctcaaccacatgctcctac 2381
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                                                                                  2382 tcacaaggactggtcgctggaactggaagtattttttcacttgatcgaga---tggaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/044,618 FILING DATE: 19930406
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08044618 Patent No. 5449605 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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STREET: 12
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                                                                                                                                                                                                                                                                                                                                        5.4%; Score 158.4; DB 1; Length 2682; 55.0%; Pred. No. 4e-37; tive 0; Mismatches 301; Indels 8;
                                                                                   REFERENCE/DOCKET NUMBER: 0654.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)466-0800
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                                                                   30,353
                                                                                                                                       TELEFAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2682 base pairs
           FILING DATE: 14-OCT-1988 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Query Match 5.4%
Best Local Similarity 55.0%
Matches 377; Conservative
                                                  NAME: FOX, SAMUEL L REGISTRATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
STRANDEDNESS: both
                                                                                                                                                                                                                                                         TOPOLOGY: linear
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US-08-044-618-3
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CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
FEARLIER APPLICATION NUMBER: US 60/088,801
FEARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 216
LENGTH: 595
                                                                                                                                                                                                                                                                                                                          ; Sequence 216, Application US/09328111; Patent No. 6262333
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-216
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
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Matches 225; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                   E: Sterne, Kessler, Goldstein & Fox 1225 Connecticut Suite 300
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BER: 0654.0490001
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APPLICATION NUMBER: US/08/044,618
FILING DATE: 19930406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/257,696
FILING DATE: 14-OCT-1988
ATTORNEY/AGENT INFORMATION:
                     Sequence 4, Application US/08044618
Patent No. 5449605
                                                                                                                                                                        POLYMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: FOX, SAMUEL L
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1592 base pairs
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MEDIUM TYPE: Floppy disk
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(202)833-8716
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Best Local Similarity 56.19
Matches 288; Conservative
                                                                                APPLICANT: SMULSON, MARK
TITLE OF INVENTION: METITIEE OF INVENTION: CANO
TITLE OF INVENTION: POLY
TITLE OF INVENTION: POLY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                                                           GENERAL INFORMATION:
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US-08-044-618-4
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2679 ggttgctttaggagacatgtatgaactaaagaaagccacgtccatggacaaacctccaag 2738
                                                           1412 AGTTGCCCTTGGAAACGTGTGTGAACTGAAGCATGCTTCACATATCAGCAAGTTACCCAA 1471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BASIE, JOHN:
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catrol, Theodore J.
APPLICANT: Porti, Adnan
APPLICANT: Porti, Adnan
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.2%; Score 125; DB 4; Length 595; 60.3%; Pred. No. 1.5e-27; ive 0; Mismatches 145; Indels
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1822 ttttacccacttgatgttgattatggtgttaagaaagcaccaaaacggaaagatatcagt 1881
                                                                                           1882 gaaatgaaaaagttetettgeteetcaattgetagaaeteatgaagatgetttteaatgtg 1941
                                                                                                                                                                       1942 gagacatatagagctgctatgatggaatttgaaawtaatatgtcagaaatgcctcttggg 2001
                                                                                                                                                                                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: GENTZ, REINER L.
APPLICANT: GENTZ, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                2002 aagctaagcmaggraaatattgagraag 2029
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/892,880 FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08892880 Patent No. 5942417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36,688
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2313 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
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STRANDEDNESS: single
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-892-880-1/C
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STATE: DC
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US-08-892-880-1
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              2708 agaaagccacgtccatggacaa---acctccaagaggaagcattcgaccaagggattag 2764
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                                                    110 TAGAGGCCAATCCTAAGGCCGAAGGATTGCTTCAAGGTAAACATAGCACCAAGGGGCTGG 51
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APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVERTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Best Local Similarity 3.6%; Pred. No. 9.5e-08;
Matches 14; Conservative 227; Mismatches 147;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,46
                                                                                                                                                                                                            US-08-232-463-14/c

Sequence 14, Application US/08232463

Patent No. 5670367
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SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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STRANDEDNESS: single
                                                                                         2765 gcaaaaccgtgcc 2777
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                                                                                                                                 50 GCAAGATGGCTCC 38
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Townsend and Townsend and Crew
51.6%; Pred. No. 4.5; tive 0; Mismatches
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REGISTRATION NUMBER: 38,498
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FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08331398A Patent No. 5608039 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-5600
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Cha
TITLE OF INVENTION: and Their I
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David
  Best Local Similarity 51.6%
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 336 base pairs
TYPE: nucleic acid
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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STATE: California
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US-08-331-398A-22
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CITY: S
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                      Matches
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                                                                                                                                                                                                                                                            2051 AAATATCAAAACTGAAAAAATAGCTTCCCAGATAGCGTTCTACTATGTGCAATTTTTG 1992
                                                                                                                                                                                                                                                                                                       252l ggaattettagteaagggetaagaattgeaceteetgaggeaeetgttaetggetatatg 2580
                                                                                                                                                                                                                                                                                                                                                 1991 AGGAATAATATTCAATTACAGAGTGTAATACCTTGCACAGCACTTGACATATAGTAGTAGCTA 1932
                                            Ouery Match
Best Local Similarity 50.0%; Pred. No. 0.18;
Matches 98; Conservative 0; Mismatches 98; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Glazer, Peter M.
TITLE OF INVENTION: TREATMENT OF HEMOGLOBINOPATHIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: OROCAPHARM, Inc.
STREET: 200 Perry Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/473,845
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
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PCT-US96-09430-7
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STATE:
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1006 aagaagaagtggcaaattccacatggaacaaagaatgattaccttatgaagtggttcaaa 1065
                                                                                                                                                                                          1066 teteaaaaggttaagaaaceagagggttetteeaceaatgteacetgagaaatetgga 1125
                                                                                                                                                                                                                               5048 AAGGIGAACCAIGAAAIGGCAIAITIGCAAACCAAAIAITICIIAAAIAIITIGGITAAI 5107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single Chain B3 Antibody Fusion Proteins
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76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Their Uses (as amended)
                                                                                                                                                                                                                                                                                                                        1126 agtaaagcaactcagagaacatcattgctgtcttcta 1162
                                                                                                                                                                                                                                                                                                                                                                5168 AATAAAAAAATTAAAAAGAAAAATCCTGCCATTTA 5204
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DB 5; Length 6060;

Score 35.4;

1.2%;

Query Match

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1457 ctgtcactgttaaagttaagggccgaagtgcttgttcatyaagtcctcyggtttgcaaga 1516
                                                                                        1517 atactgotcacattcottragratgggaaaagcatatacaatgcamcottaaacatgtto 1576
                                                                                                                  ; LOCATION: 1..336
; OTHER INFORMATION: /note= "B5 Variable Light chain (V-L)"
US-08-759-804A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor-Specific Antibody Fragments, Fusion Proteins, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Weber, Ellen L. REGISTRATION NUMBER: 32,762 REFERENCE/DOCKET NUMBER: 015280-126140US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-CCT-1994
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-CCT-1990
FILING DATE: 12-CCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/759,804
FILING DATE: 03-DEC-1996
                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08759804A Patent No. 5990296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pestan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pal, Lee
TITLE OF INVENTION: Fusion Protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 336 base pairs
nucleic acid
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                   155 TGATCT 160
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FEATURE:
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                                                                                                                                                                                                                                                                              RESULT 11
US-08-759-804A-22
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                                                         1457 ctgtcactgttaaagttaagggccgaagtgcttgttcatyaagtcctcyggtttgcaaga 1516
                                                                                                                                                            0; Gaps
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                                                                                                 35 CTGTCAGTCTTGGAGATCAAGCCTCTATTTCTTGTAGATCTAGTCAGAGCATTGTACATA 94
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; OTHER INFORMATION: /note= "B5 Variable Light chain (V-L)"
US-08-331-3978-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 1.2%; Score 35.2; DB 2; Length 336; I Similarity 53.2%; Pred. No. 0.8; 67; Conservative 3; Mismatches 56; Indels
                     56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One Market Plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Townsend and Townsend and Crew
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3; Mismatches
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-0CT-1990

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                           US-08-331-397B-22; Sequence 22, Application US/08331397B; Patent No. 5981726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
Best Local Similarity 53.2%;
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Market P
CITY: San Francisco
STATE: California
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                             155 TGATCT 160
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Query Match

JS-09-227-693-22

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1457 ctgtcactgttaaagttaagggccgaagtgcttgttcatyaagtcctcyggtttgcaaga 1516
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                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                          35 CTGTCAGTCTTGGAGATCAAGCCTCTATTTCTTGTAGATCTAGTCAGAGCATTGTACATA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FitzGerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv
                                                                Length 336;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
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                                                                                                        3; Mismatches 56;
                                                                DB 4;
                                                                Score 35.2; DI
Pred. No. 0.8;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/331,398A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 60, Application US/08331398A Patent No. 5608039 GENERAL INFORMATION:
APPLICANT: Pastan, Ira APPLICANT: Willingham, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                Query Match 1.25
Best Local Similarity 53.25
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 375 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE: 28-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA
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STRANDEDNESS:
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                                                                             1457 ctgtcactgttaaagttaagggccgaagtgcttgttcatyaagtcctcyggtttgcaaga 1516
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                                                                                                                                                                                        Gaps
                                                                                                        APPLICANT: BENHAR, Ital
APPLICANT: PADLAN, Eduardo A.
APPLICANT: JUNG, Sun Hee
APPLICANT: JUNG, Sun Hee
APPLICANT: LEE, Byungkook
TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
1.2%; Score 35.2; DB 2; Length 336; 53.2%; Pred. No. 0.8; ive 3; Mismatches 56; Indels
                                          56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
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variable light chain"
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APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/227,693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09227693
Patent No. 6287562
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 32,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                   Local Similarity 53.2
nes 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 336 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1..336 OTHER INFORMATION: /sta OTHER INFORMATION: vari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PASTAN, Ira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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California
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APPLICANT:
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                                                                                                      0; Gaps
                                                                                                                                                                                    Query Match
Best Local Similarity 53.2%; Pred. No. 0.86;
Matches 67; Conservative 3; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Tumor-Specific Antibody Fragments, TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
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03-DEC-1996
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APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMBER: US 07/767,331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Weber, Ellen L. REGISTRATION NUMBER: 32,762
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Pai, Lee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pastan, Ira
Willingham, Mark
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EDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
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Light chain region"
                                                                                             Query Match
Best Local Similarity 53.2%; Pred. No. 0.86;
Matches 67; Conservative 3; Mismatches 56; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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One Market Plaza, Steuart Street Plaza
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OTHER INFORMATION: Light chain region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA: US 07/596,289
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 38,498
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APPLICANT: Benhar, Itai
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CORRESPONDENCE ADDRESS:
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California
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OTHER INFORMATION:
OTHER INFORMATION:
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US-08-331-398A-60
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; NAME/KEY: -
; LOCATION: 1.375
OTHER INFORMATION: /note= "Mouse monoclonal antibody B5 Fv OTHER INFORMATION: Light chain region"
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0; Ouery Match Best Local Similarity 53.2%; Pred. No. 0.86; Matches 67; Conservative 3; Mismatches 56; Indels 0; Gaps

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ψ.	٠, ١	٠,			AV834168 AV834168	BE420229 WWSU4.CII	BE941860 EST421439		0,		AA401836 zv66b12.r
SUMMARIES	B ID	. ~.	10 AV833309	11 BF255013	10 BE419432	10 BE516130	10 AV834168	10 BE420229	11 BE941860	11 BF459972	11 BG042229	13 AQ577141	10 AA401836
	Query Match Length DB	653	714	209	536	427	661	369	419	674	502	759	699
æ	Query Match 1	19.7	16.4	11.5	10.6	10.2	10.1	9.1	7.6	7.5	6.4	6.3	6.1
	Score	579.8	484.6	338.2	312	301.8	299	269.2	223.8	221	189	186.2	181
	Result No.	1	2	m	4	י גר	0	7	œ	σ	, 0	::	12

// Conganism="zea mays"
/cultivar="11linois High Oil"
/db_xref="taxon:4577"
/clone_lib="687"
/tissue_lype="embryo"
/dev_stage="14, 21, 28, and 35 days after pollination"
/lab_host="E. coli SOLR"

0.4.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0	861         11         BG280821         BG280821           9 16         11         BIO93436         BIO93436           8         99         11         BG031594         BG031594           5         728         10         AI455188         AI455189           5         651         10         AV833893         BG429402           6         10         AV833893         BIO91452         BIO91452           4         834         11         BF101770         BF101745           3         617         10         AA212857         AA212857           3         617         10         BE911127           3         587         11         BF911127	2         560         11         BF042005         BR550013A           2         560         11         BG751755         BG816404         BG816404         BG816404         BG816404         BG816404         BG816404         BG816404         BG816404         BG816404         BG81651755         BG816404         BG816404         BG81661641         BG81661164         BG81661166         BG81661164         BG816611164         BG8166	ALIGNMENTS 653 bp mRNA y1 687 - Early embryo from Del GI:6021377	idiplantae; Streptophyta; Embryophyta Magnoliophyta; Liliopsida; Poales; P Gaae; Andropogoneae; Zea. 653) m various CDNA libraries sequenced at 1999)	The many control of the control of con
0.4.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0 % 0.0	ดพพพพพพพพพพพ แผ่ตพพพพสสมพพพ	, , , , , , , , , , , , , , , , , , ,	105 )D02. 1Ce. 805 805.1	a; pph an an try try	Contract. The property of the
	113 1144 116 118 119 119 120 133	77777777777777777777777777777777777777	N ON SM	ലംഗ ച	٥

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae

Hordeum vulgare subsp. vulgare. Hordeum vulgare subsp. vulgare

ORGANISM

SOURCE

Triticeae; Hordeum. (bases 1 to 714)

Sato, K.

REFERENCE AUTHORS TITLE JOURNAL

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/

Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission;

database:http://www.shigen.nig.ac.jp/barley/Barley.html.

Location/Qualifiers

FEATURES

a o 9 0 0 Q D 8 6 8

Q Q

/organism="Hordeum vulgare subsp. vulgare"

/cultivar="Haruna Nijo" /db_xref="taxon:112509"

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/note="Organ: embryo: Vector: pBluescript SK; Site_1: xhoI : Site_2: EcoRI; Library was prepared by Statagene using the Uni-ZaP xR system (Stratagene BN937328-12). Clones were picked by a clobe after blue/white selection (ampicillin resistance - use 100 micrograms/microliter). Developed from a pool of equal amounts of RNA from developing embryos sampled at 14, 21, 28 and 35 days after pollination of the Illinois High Oil Maize Strain Cycle 90. This closed strain has been selected for high oil concentration for 90 generations and originates from the 1890s era open pollinated variety Burr's White"
                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1661 agtggggacgggttgggggtgagaaattggagggcaaaaactggaggagatgtcaaaaa 1720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2021 ttgagraaggatttgaagcattaactkrgrtacmgratttatttgaaggacaccgctnat 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2141 tatcccttctattcatcctcatattatacgggatgaggatgatttcatattcaaaggcga 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                           DB 10; Length 653;
                                                                                                                                                                                                                                                                                                                              6; Indels
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19.7%; Score 579.8; DB 10;
Best Local Similarity 96.0%; Pred. No. 7.3e-139;
Matches 616; Conservative 16; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="bags5k04"
/clone_lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare shoots germination"
/tissue_type="shoots"
/dev_stage="germination"
121 c 162 g 182 t
                                                                                                                                                                                                                                                                                                                                                      1645 tgctacgtatttcgtaagtggggacgggttgggaagtgagaaaattggagggcaaaactg 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1825 tacccacttgatgttgattatggtgttaagaaagcaccaaaacggaaagatatcagtgaa 1884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                      244 GGAAACCCCTGGGAAGCATGGGAACAAAAACAAATTTTCAGAAGCAGCCTGGGAGATTT
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                                                                                                                                                  tch 16.4%; Score 484.6; DB 10; Length 714; al Similarity 82.3%; Pred. No. 2.9e-114; 587; Conservative 19; Mismatches 102; Indels 5;
                                                                                                                                                    Query Match
Best Local Similarity
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AV833309 714 bp mRNA EST 22-JUN-2001
AV833309 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgare shoots germination Hordeum vulgare subsp.
clone bags5k04, mRNA sequence.

DEFINITION

AV833309

RESULT

ACCESSION

VERSION KEYWORDS

AV833309.1 GI:14525398 EST.

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE419432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                 BF255013 607 bp mRNA EST 23-FEB-2001 HVSMEf0005L18f Hordeum vulgare seedling root EST library HVcDNA0007 (etiolated and unstressed) Hordeum vulgare cDNA clone HVSMEf0005L18f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2509 acgaattitgtgggaattettagteaagggetaagaattgeacetectgaggeacetgtt 2568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Hordeum vulgare seedling root EST library HVcDNA0007 (etiolated and unstressed)" /tissue_type="Seedling root"
                                                                     atssytttttcactcttatcccttctattcatcctcatattatacgggatgaggatgatt 2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACAAATTTATTGGAATTCTTAGTCAAGGACTAAGGATAGCACCTCCTGAGGCACCGGG 60
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                                                                                          643 GGATGACACTGGCAATCAAGAACTGGC-TCTTAGAGAGCTTGATTGTTGTTGCTGCAAGCA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for barley genomics mobilished (2000) on Nov 16, 2000) this sequence version replaced gi:11184130 Contact: Wing RA
                                                                                                                                                        2185 tcatattcaaaggcgaaaatgcttgaagctctgcaggatattgaaattgcttc 2237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.5%; Score 338.2; DB 11; Length 607; 85.6%; Pred. No. 1.9e-76;
                                                                                                                                                                                662 TGACAATGAAA-GCGAAAATGCTTGAAGCTCTTCAGGATATTGAAATTGCTTC 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Hordeum vulgare"
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/clone="HVSMEf0005L18f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@clemson.edu
Seq primer: AATAACCCTCACTAAAGGG
High quality sequence stop: 551.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                     BF255013
BF255013.2 GI:13117445
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
1 (bases 1 to 536)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson.O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Fermann,R.G., Holton,T., Jacquenin,J.M., Jia,J., Joudrier,P., Largidge,P., Lazo,G.R., Lin,J.J., McGuire,P., Oghhara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorcells,M., Warbbuton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="WWS012.Al2"
/clone_lib="ITEC WWS Wheat Scutellum Library"
/tissue_type="scutellum callus"
/note="Wl3 Reverse sequencing primer used for 5' end of
                                                                                                                                                                                          2689 ggagacatgtatgaactaaagaaagccacgtccatggacaaacctccaagagggaagcat 2748
                                                                                                                                                                                                                                                                                        2809 gatgtcgtagttccctgcggcaagccggtgccatcatcaattaggagctctgaactcatg 2868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE419432 536 bp mRNA EST 24-JUL-200 WWS012.A12R000101 ITEC WWS Wheat Scutellum Library Triticum aestivum cDNA clone WWS012.A12, mRNA sequence.
                                                                                                                                    Zeneca Wheat Improvement Centre, Norwich Research Park
Colney Lane, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 250 2600
Fax: 44 1603 250 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 312; DB 10; Length 536;
Pred. No. 1.1e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: wolfgang.schuch@aguk.zeneca.com
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://wheat.pw.usda.gov/genome
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85.1%;
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Contact: Schuch W
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1 (bases 1 to 427)
Anderson, O. D., Chao, S., Han, P. S., Hsia, C. C., Johnson, R. R., Kang, Y., Lazo, G. R., Miller, R., Rausch, C. J., Seaton, C. L., Tong, J. C., Verhey, S. D. and Walker-Simmons, M. K.
The structure and function of the expressed portion of the wheat genomes - ABA-treated embryo library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Seed embryo"
/dev_stage="Mature dormant seeds"
/dab_host="E. coli DH12s"
/note="Vector: pGAD10; Site_1: EcoR1; Site_2: XhoI;
Embryos were cut from mature, dormant seeds and imbibed in
                                     2539 ctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctctac 2598
                                                                                                                        2599 tttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcctgta 2658
                                                                                                                                                                                                                                                                                                                                                                        2719 tccatggacaaacctccaagaggaagcattcgaccaagggattaggcaaaaccgtgcca 2778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHE612_D07_H142A Wheat ABA-treated embryo cDNA library Triticum aestivum cDNA clone WHE612_D07_H14, mRNA sequence.
                                                                                                                                           /cultivar-"Brevor (soft, white, winter, common wheat)"
/db_xref-"taxon:4565"
/clone-"WHE612_D07_H14"
/clone_llb-"Wheat ABA-treated embryo cDNA library"
      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 CCAGCATCTATCANGGCATCTGAGCTTCTGTACAACGAGTATATAGTCTACAACAAGGC 364
                                                                 08-AUG-2000
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Email: candersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Clontech Matchmaker 3' AD primer.
                                                                                                                                                                                                                                                                                                                                 185 CCAATGGACAAACCTCCAAGAGGAAAGCATTCGACCAAGGGCTTAGGAAAAACTGTGCCG
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  0; Mismatches
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25 microM ABA (abscisic acid) in 5 mW Mes buffer, pH 5.7, fC 12 hr at 22 C. The tissue, total RNA, and poly(A) RNA were prepared by Steven Verhey in M.K.
Walker-Simmons's lab (USDA-ARS, Washington State Univ., Pullman, Washington 99164-6420. A cDNA library was made by Clontech using a combination of random and oligo dT primers Library was plated and archived by Russell Johnson (Colby College, ME/Walker-Simmons' lab). Plasmid DNA preparations and DNA sequencing were performed in the 93 c. 84 g 128 t
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2228 aaattgottcaaagatagttggottcgatagcgacagtgatgaatctottgatgataaat 2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2348 ttgagcagtatctcctcaacacacatgctcctactcacaaggactggtcgctggaactgg 2407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2408 aggaagtttttcacttgatcgagatggagaacttaataagtactcaagatataaaaata 2467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OKAyama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@iib.okayama-u.ac.jp/barley/
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct
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Pred. No. 4.4e-67;
6; Mismatches 53; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Kazuhiro Sato
Research Institute for Bioresources
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85.0%;
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWS04.C11R000101 ITEC WWS Wheat Scutellum Library Triticum aestivum cDNA clone WWS04.C11, mRNA sequence.
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International Triticae EST Cooperative (TEC): Production of Expressed Sequence Tags for Species of the Triticae
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2781 ggagtcagagtttgtgaagtggagggatgatgtcgtagttccctgcggcagccggtgcc 2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2841 atcatcaattaggagctctgaactcatgtacaatgagtacatcgtctacaacacatccca 2900
                                                                                                                                                                                                                                                                                                                                                                                  2721 catggacaaacetecaagagggaagcattegaccaagggattaggeaaaaccgtgecact 2780
                                                                                                                                                                                                                                                                                                                  2542 agaattgcacctcctgaggcacctgtta-ctggctatatgttcggcaaaggcctctactt 2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AGCATCTATCAGGGCATCTGGAGCTTCTGTACAGGGTATATAGTGTACAACACAGGTCA 302
                                                                 /cultivar="Haruna Nijo"
/cultivar="Haruna 112509"
/clone="rbags5k04"
/clone_lib="K. Sato unpublished cDNA library: Hordeum
                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       database:http://www.shigen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
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                                                                                                                                                                                                                                            Score 299; DB 10; Length 661;
Pred. No. 2.6e-66;
0; Mismatches 60; Indels 1
                                                                                                                                vulgare subsp. vulgare shoots germination"
/tissue_type="shoots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                    /dev_stage="germination"
181 c 132 g 168
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Similarity 85.0%;
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Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Cote, F., Ojanen-Reuths, T., Hahn, M.G., VandenBosch, K., Hur, J.,
Beremand, P., Craven, M.B. and Cho
Beremand, P., Endre, G., Town, C.D., Bowman, C.L., Craven, M.B. and Cho
, J., Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTS from seedling roots of Medicago truncatula after treatment with beta glucan elicitor preparation from Phytophthora sojae
                                                                                                                                                                                                                                                   /clone="WWSO4.C11"
/clone_lib="ITEC WWS Wheat Scutellum Library"
/tissue_type="scutellum callus"
/note="M13 Reverse sequencing primer used for 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2719 tecatggacaaacetecaagagggaagcattegaceaagggattaggeaaaacegtgeea 2778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2599 tttgcagatctagtaagcaagagcgcacaatactgttatgtggataggaataatcctgta 2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2539 ctaagaattgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctctac 2598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 03-OCT-2000 EST 03-OCT-2000 EST421439 MGHG Medicago truncatula cDNA clone pMGHG-6B18, mRNA secure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 CTAGAGTCGGAGTTTGTGAAATGGAGGATGATATCGTCGTGCCTTGTGGCAAGCCAGTG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 269.2; DB 10; Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.1e-58;
Mismatches 53; Indels
                                                             Email: wolfgang.schuch@aguk.zeneca.com
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
Colney Lane, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 250 2600
Fax: 44 1603 250 699
                                                                                                                                                                                                      /cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
                                                                                                                                                                                 /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                             87 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                          Spermatophyta, Magnollophyta, endicotyledons, core eudicots, Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

(bases I to 674)

Nielsen, K.L. Crookshanks, M., Emmersen, J. and Wellinder, K.G. EST-sequencing of mature potato tuber (var. Kuras)

Unpublished (2000)

Contact: Karen G. Wellinder

Institut for bioteknologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mature_tuber lambda ZAP"
/tissue_type="Tuber"
/note="Vector: Lambda ZAP"
                                                                                                                                                                                                                                                                   Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Field grown Kuras"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 674
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                BF459972.1 GI:11529129
                                                                                                                                                                                                                                                                                                                                              Email: kgw@bio.auc.dk
                                                                            tuberosum
                                                                                                                                                                                                                                                                                                         Tel: +45 96358467
Fax: +45 98141808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    POLYA-No.
                                                                            Solanum
                                                          potato.
                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: Daluescript SK-; Site_1: EcoRI; Site_2: Mole="Vector: Paluescript SK-; Site_1: EcoRI; Site_2: Mole; CDMA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unizap Rx vector from Strategene and packaged using digapack III Gold packaging from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF459972 674 bp mRNA EST 04-DEC-2000 071B10 Mature tuber lambda ZAP Solanum tuberosum cDNA 5' similar to NAD+ ADP-ribosyltransferase (EC 2.4.2.30) [imported]. . . pir|T51353, BF459972
                                                                                                                                                      University of Georgia name: G269712e TIGR sequence name: MTJAP09TK More information is available at: http://chrysie.tamu.edu/medicago Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2368 acacatgctcctactcacaaggactggtcgctggaactggaggaagttttttcacttgat 2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2428 cgagatggagaacttaataagtactcaagatataaaaataatctgcataacaagatgcta 2487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctagtaagcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatg 2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2668 ctictitctgaggitgctttaggagacaigiatgaactaaagaaagccacgiccaiggac 2727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AGAGAAGGTGAATAAGATCAATATGCCCGTTACAGAGACAAAGTAGGCAACAGAATGCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2728 aaacciccaagaggaagcaiicgaccaagggaitaggcaaaaccgigccaciggagic 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib-"MGRG"
/clone_lib-"MGRG"
/clsue_type="Roots from four day old seedlings"
/dev.stage="2 days after treatment with beta glucan elicitor preparation from Phytophthora sojae"
/lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 223.8; DB 11; Length 419; 70.9%; Pred. No. 6.2e-47; tive 0; Mismatches 122; Indels 0;
                                                                              220 Riverbend Road, Athens, GA 30602-4712, USA
                                                                                                                                                                                                                                                     /organism="Medicago truncatula"
                Contact: Michael G. Hahn
Complex Carbohydrate Research Center
                                                                                                                                                                                                                                                                                           /db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                 /clone="pMGHG-6B18"
                                                                                                                                    Email: hahn@ccrc.uga.edu
                                                                                                                                                                                                                                                                           /cultivar="A17"
                                                          University of Georgia
    Unpublished (2000)
                                                                                                Tel: 706-542-4457
Fax: 706-542-4412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 70.9
Matches 297; Conservative
                                                                                                                                                                                                                                       419
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1215 aaatgagtggattgagaagctcaaacttgctggtgccaacttctatgccagggttgtcaa 1274
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                                                                                                                                                                                                                                                                                                                  68 AGACACAGATTGCTTAGTTGTAATAGGGACGTGGAATGATCAAGATTCTGAGATAAAGAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                           128 GGCCAGGAGTGAAAGTGCCAGTAGTCAGGGAGGATATTTGGTGGATAGTATCAACAG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 GAA----AACTGTCAAAGTAAAAGGGAGGAGTGC--GGTTCATGAGTCATCCAAATTGGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 AG-ATACAGGACACATT-CTTGAGGACAAGACCAGCATTTATAATACGACTTTAAATATG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggcaaaaactggaggagatgtcaaaaactgaggcaatcaaggaattcaaaagattatttc 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 -TCAGACCTCTCAAGTGGCATTAATA-GTTACTACATCCTTCAAATTATTGAAGAGGACA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 537
                                                                                Gaps
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                                                                                                                                                                                     8 AGAGAACTGGAAGAAGAAATTGAGGAAGCTGGTGGACGGGTGCATGCCAAGTTGAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
tch 7.5%; Score 221; DB 11; Length 674; al Similarity 64.8%; Pred. No. 3.7e-46; 428; Conservative 5; Mismatches 217; Indels 1:
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AQ577141.1 GI:4977626
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                                                                                                  Matches 243; Conservative
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                                         Query Match
Best Local Similarity
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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//note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
Xho1; The cDNA library was constructed from mRNA isolated
from mature seed pods of greenhouse grown plants prior to
senescence for the cultivar KPI. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
poly(dT) sequence with a XhoI restriction site. EcoRI
poly(dT) sequence with a Complement of the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                          BG042229 502 bp mRNA EST 31-JUL-2001 su93c12.yl Gm-c1055 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: Gm-c1055-2064 5' similar to TR:Q9ZP54 Q9ZP54 POLY(ADP-RIBOSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Missouri 63134 For further information
Farkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 502)
Shoemaker, K. Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna Shoemaker,R., Keim,P., Vodkin,L., Kucaba,T., Martin,J., Beck,C., A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                1814 ctgggagattttacccacttgatgttgattatggtgttaagaaagcaccaaaacggaaag 1873
                                                                                                                                      598 CIGGCAGATITIATCCTCTGGATATIGATTATGGGGGTTGACAAAAAAACCACCTCTAAG 657
Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_1bb-"GENOME SYSTEMS CLONE ID: Gm-c1055-2064"
/clone_lib-"Gm-c1055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        info@genomesystems.com web site: www.genomesystems.com Insert Length: 429 Std Error: 0.00 High quality sequence stop: 419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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BG042229
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ACCESSION

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KEYWORDS VERSION SOURCE REFERENCE AUTHORS 80 C

150 a

BASE COUNT

FEATURES

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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/clone_lib="CGGI Rice BAC Library"
/tissue_type="Leaf"
/lab_lost="E. coli DH10B"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the world population especially those world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2855 gototgaactcatgtacaatgagtacatcgtotacaacacatcccaggtgaagatgcagt 2914
                                                                                                                                                                                                                                                                                                                                                                                               2615 gcaagagcgcacaatactgttatgtggataggaataatcctgtaggtttgatgcttcttt 2674
                                                                                                                                                                                              2675 ctgaggttgctttaggagacatgtatgaactaaagaaagccacgtccatggacaaacctc 2734
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                                                                                                                                                                                                                                           62 GTGAAGTTGCGCTTGGAAATGTCTATGAGCTCAAGAAAGCTAAGTATATGGATAAACCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ577141 759 bp DNA GSS 02-JUN-1999
nbxb0090B07r CUGI Rice BAC Library Oryza sativa genomic clone
nbxb0090B07r, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUN-1999
                                                                                                                                    Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
                                                    .;
0
6.4%; Score 189; DB 11; Length 502; 73.0%; Pred. No. 6.3e-38; tive 0; Mismatches 90; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 404. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4530"
/clone="nbxb0090B07r"
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carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arunganathan and Barle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library contains 36.864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probablity of 99.98. Two high density filters,
each containing 18.432 clones (doubly spotted), represent
the whole library for colony screening.

229 a 148 c 174 g 207 t lothers
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ó; 570 taagggttccaagcgcaagaaaagtgaaaatgatattgatagctacaaatccgccaggtt 629 630 agatgaaagtacatctgaaggtacagtgcgaaacaaagggcaacttgtagacccacgtgg 689 296 AATCAGGAGTATATCAGAAGGCACAGCAGAAGATAAAGGGAAAGCTGTTGTATCACATGA 355 ttccaatactagttcagctgatatccaactaaagcttaaggagcaaagtgacacactttg 749 Gaps .; 0 DB 13; Length 759; 78; Indels 6.3%; Score 186.2; DB 1 74.9%; Pred. No. 3.7e-37; tive 0; Mismatches 78 Matches 233; Conservative 870 aatgctatttg 880 536 CATGCTATTTG 546 Best Local Similarity Query Match 750 ö ò g g ô q ò a ð

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 669)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., T., Waterston,R. and Willoso,R., Tan,F., Theising,B., White,Y., Wylie Washlw Merck EST Project 1997
                                                   zv66b12.rl Soars_total_fetus_Nb2HP8_9w Homo sapiens cDNA clone IMAGE:758951 5' similar to 9b:J03473 NAD(+) ADP-RIBOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
                                                                                                                                                               AA401836.1 GI:2055855
                                                 dq 699
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                       Homo sapiens
                                                 AA401836
                                                                                                                                                                                                                 human.
RESULT 12
                                                                  DEFINITION
                                                                                                                                                                                                                                  ORGANISM
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COMMENT
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                               AUTHORS
                        AA401836
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2816 tagiteceigeggeaageeggigeeateateaattaggageietgaacteatgiacaaig 2875

537 ACGIICCICITGGGACCGGGAITICAICIGGIGIGAAIGACACCICTACIAIATAAACG 596

op

480 AAGGTTTGGGCAAAACTACCCCTGATCCTTCAG---CTAACATTAGTCTGGATGGTGTAG 536

2876 agtacatcgtctacaacacatcccaggtgaagatgcagttcttgctgaaggtgcgtttcc 2935

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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pYT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 152 c 157 g 169 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5;
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2276 ttgatgataaatatatgaaacttcactgtgacatcacccgctggctcacgatagtgaag 2335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2336 attacaagttaattgagcagtatctcctcaacacacatgctcctactcacaaggactggt 2395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2456 gatataaaaataatctgcataacaagatgctattatggcacggttcaaggttgacgaatt 2515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 CCTTT---AAGCAGCTTCATAACCGAAGATTGCTGTGGCACGGGTCCAGGACCACCACT 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2636 atgiggataggaataatccigtaggittgaigctictitctgaggitgciitaggagaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 181; DB 10; Length 669;
Pred. No. 7.9e-36;
0; Mismatches 285; Indels (
                                                                                                                                                                                                  /clone_lib="Soares_total_fetus_Nb2HF8_9w"
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/lab_host="DH10B"
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                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:758591"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.1%;
Best Local Similarity 56.5%;
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BI093436.1 GI:14511766
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BI093436
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue.type="melanoft" melanoma" /tissue.type="melanoft" melanoma" /lab_host="DH10B" (phage resistant)" /lab_host="DH10B" (phage resistant)" /note="Organ: skin; vector: pOTB7; Site_1: xhoI; Site_2: /note="Organ: skin; vector: pOTB7; Site_1: potB7 made by oligo dr priming. Directionally ECOR; consd into ECORI/XhoI sites using the following 5, cloned into ECORI/XhoI sites using the following 5, cloned into ECORI/XhoI sites relected >500bp for average adaptor: GGCACAGG(G). Library constructed by Ling Hong in insert size 1.8kb. Library constructed by Ling Hong in insert size 1.8kb. Library constructed by Ling Hong in closert size 1.8kb. Missing ZAP-CDNA synthesis kit california, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 GAGGGCTGATGATAGCAGCAAGGATCCCATCGATGTCAACTATGAGAAGCTCAAAACTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.F. Consortium/LLNL at: image.llnl.gov
plate: LLCM1225 row: c column: 18
High quality sequence stop: 825.
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                                                                                                                                                                                                                  602401166F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4543433 5',
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Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
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56.0%; Pred. No. 9.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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602859629F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:5000911 5',
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11033 row: i column: 08
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                                                                                    2546 tigcacciccigaggcaccigitaciggciataigticggcaaaggccictactigcag 2605
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533 TCCTGTTGGGAAGTTGCCCTTGGAACATGTATGAACTGAAGCACGCTTCACATATCA 592
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                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc.
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Location/Qualifiers
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Tissue Procurement: ATCC
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM10089 row: m column: 09

Tissue Procurement: DCTD/DTP

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/clone_lib="NIH_MGC_87" /clone="IMAGE:4394288"

High quality sequence stop: 678. Location/Qualifiers

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Source

FEATURES

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NIH-WGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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Average insert size 1.5 kb. Library prepared by Life
                                                                                                                                                                                                                                           64 GAAGTATGTTAAGAACACTCATGCAACCACACAATGCGTATGACTTGGAAGTCATGGA 123
                                                                                                                                                                                                                                                                                                         124 TATCTTTAAGATAGAGGGTGAAGGGGAATGCCAGGGTTACAAGGCGTTTAAGGAG---CT 180
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                                                                                                                                     6; Gaps
                                                                                                                                                                                                                                                                                                                                                              241 ccaggeretregearaccececereaagececereacagecracaterregradas 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2712 agocacgtccatggacaaacctccaagagggaagcattcgaccaagggattaggcaaac 2771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG031594 990 bp mRNA EST 24-JAN-2UU1
602299739F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4394288 5',
                                                                                                                                                                                4 GAAGCTCAAAACTGACATTAAGGTGGTTGACAGAGTTCTGAAGAAGCGGAGTCATCAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GATCTATTTCGCTGACATCTCCCAAGAGTGCCAACACTCCCGTATCTCAGGAGA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2772 cgtgccactggagtcagagtttgtgaagtggagggatgatgtgcgtagttccctgcggcaa 2831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2832 geoggigocalcalcaallaggageletgaaetealgiacaalgagiacalegictacaa 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 cécticacatatrescaagetracceaagecaageageteteaagetriggecaaaac 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 TACCCCTGATCCTTCAG---CTAACATTAGTCTGGATGGTGTAGACGTTCTTCTTGGAC 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       538 CGGGATTICATCTGGTGTGAATGACACCTCTTACTATAAACGAGTACATTGTCTATGA 597
                                                                                            5.9%; Score 174.6; DB 11; Length 916; 56.4%; Pred. No. 3.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.8e-34;
0; Mismatches 279; Indels
                                     229 t
                              230 g
               Technologies.
209 c
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                                                                                                                  Matches 368; Conservative
                                                                                   Query Match
Best Local Similarity
                           248 a
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                      BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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/tissue_type="manmary adenocarcinoma, cell line"
//dab_host="hHi0B (phage-resistant)"
//act_bost="hHi0B (phage-resistant)"
Site_2: SalI; Cloned unidirectionally: oligo-dr primed.
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                   2247 tggcttcgatagcgacagtgatgaatctcttgatgataaatatatgaaacttcactgtga 2306
                                                                                                                                                                                                                                                                                                                                       2307 catcaccccgctggctcacgatagtgaagattacaagttaattgagcagtatctcctcaa 2366
                                                                                                                                                                                                                                                                                                                                                                                                             2367 cacacatgctcctactcaccaaggactggtcgctggaactggaagtatttttcacttga 2426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2427 togagatggagaacttaataagtactcaagatataaaaatatcgcataacaagatgct 2486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2487 attatggcacggttcaaggttgacgaattttgtgggaattcttagtcaagggctaagaat 2546
                                                                                                                                                                                                                                                                                                                                                                          68 CATTAAGGTGGTTGACAGAGTTCTGAAGAGCCGAGATCATCAGGAAGTATGTTAAGAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2547 tgcacctcctgaggcacctgttactggctatatgttcggcaaaggcctctactttgcaga 2606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2607 tctagtaaggaagggggacaatactgttatgtggataggaataatcctgtaggtttgat 2666
                                                                                                                                                                                                                                                                                                                                                                                                                                                128 CACTCATGCAACCACACACAATGCGTATGACTTGGAAGTCATCGATATCTTTAAGATAGA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 GCGTGAAGGCGAATGCCAGCGTTACAAGCCCTTT----AAGCAGCTTCATAACCGAAGATT 244
                                                                                                                                                                                                                                                  7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2727 caaacctccaagagggaagcattcgaccaagggattaggcaaaaccgtgccactggagtc 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2787 agagtttgtgaagtggaaggatgatgtcgtagttccctgcggcaagccggtgccatcatc 2846
                                                                                                                                                                                                                                                                                                      8 regercreargarageascaacsarccarccarccaacrargasaascreaaacrea 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 AGCCCCGCCTGAAGCGCCCGTGACAGGCTACATGTTTGGTAAAGGGATCTATTCGCTGA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 CCTGTTGGGAGAAGTTGCCCTTGGAAACATGTATGAACTGAAGCACGCTTCACATATCAG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           485 CAAGTTACCCAAGGCAAGCACAGTCTAAAGGTTTGGGCAAAACTACCCTGATCCTTC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        545 AG---CTAACATTAGTCTGGATGGTGGTAGACGTTCCTCTTGGGACCGGGATTTCATCTGG 601
                                                                                                                                                                                                   Score 170.8; DB 11; Length 990;
Pred. No. 3.7e-33;
0; Mismatches 302; Indels 7;
                                                                                                                                                                                                     5.8%;
                                                                                                                                                                                                                                  389; Conservative
                                                                                                                                                                                                               Best Local Similarity
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov

TITLE

COMMENT

REFERENCE

AUTHORS

Search completed: March 7, 2002, 15:24:26 Job time: 3336 sec

